



379 AGCAGCGTGAAGAGGGGGCCCAAGCACCTCTTGATCTGGAGTCTTGTTCGAGCA 438  
301 GUCAUACGAAGAAGUUCGGACCCUGUGGCUUCCUGUGUGAAGUACCGCGCGC 360  
439 GTAATCACTAAGAAGTGGCTGATTGGTTGGTTTCTGTCTCTCAATATCGAGCCAGG 498  
361 GAGCGGUCACGAAGCGGAGUUCUGAGGAGCGUACUACGAAGUACGAGCUUC 420  
499 GAGCAGTCAAAAGGAGAAATCTGGAGAGTCTCAAAAATTAAGACACTGTGTTT 558  
421 CCGGAGAUUUCCGAAGCGGAGAGAGCAGCAGCUGGUGUUCGCGAUCGAGCUAAG 480  
559 CTTGAGATCTTCGCAAGCTCTGAGTCTTGAGTCTTGAGTCTTGAGTCTTGAGT 618  
481 GAGCGGACCGGACCGGACAGCUACGUGUGUACGUGGCGGCGGCGGCGGCGGCG 540  
619 GAAGCAGACCCACCGGACCTCTATGTCTCTGACCTGAGTCTCTCTATGAT 678  
541 GGCUGUGGGCGACCAACAGAUACGCGGAGAGCGGCGGCGGCGGCGGCGGCGG 600  
679 GGCCTGCTGGGTGATTAATCAGATCATGCCCAAGACAGGCTTCTGATTAATGTCCTGTC 738  
601 AUGAUCGCGAUGAGGCGCGCCACGCGCGGAGGAGAGUUCUGGAGGAGCUGAGCUC 660  
739 ATGATTGCATGGAGGCGGCGCATGCTCTGAGGAGGAAATCTGGGAGGAGTGAAGTGTG 798  
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US-09-949-016-703  
; Sequence 703, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 703  
; LENGTH: 1624  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-703  
Query Match 64.1%; Score 601.6; DB 3; Length 1624;

Best Local Similarity 64.7%; Pred. No. 2 8e-85;  
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;  
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Qy 121 GGCAGCUGGAGGAGGUCGCGAGCGGCGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGG 180  
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; Sequence 2688, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:







[illegible]

RESULT 6  
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; Sequence 8, Application US/09066281B  
; Patent No. 6475783  
; GENERAL INFORMATION:  
; APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING  
; FOR TUMOR REJECTION ANTIGEN PRECURSOR  
; TITLE OF INVENTION: FOR TUMOR REJECTION ANTIGEN PRECURSOR  
; AND PAGE-C2

Query Match 64.1%; Score 601.6; DB 3; Length 1691;  
Best Local Similarity 64.7%; Pred. No. 2.8e-85;  
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

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[illegible]

RESULT 7  
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; Patent  
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM nucleic - nucleic search, using sw model  
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Perfect score: 939  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 9793542 seqs, 413469005 residues  
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA\_Main\*  
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9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES  |       |       |        |        |                      |                       |             |  |  |  |  |  |  |
|------------|-------|-------|--------|--------|----------------------|-----------------------|-------------|--|--|--|--|--|--|
| Result No. | Score | Query |        | Length | DB                   | ID                    | Description |  |  |  |  |  |  |
|            |       | Match | Length |        |                      |                       |             |  |  |  |  |  |  |
| 1          | 939   | 100.0 | 939    | 8      | US-10-729-830-10     | Sequence 10, Appl     |             |  |  |  |  |  |  |
| 2          | 806.2 | 85.9  | 939    | 8      | US-10-729-830-11     | Sequence 11, Appl     |             |  |  |  |  |  |  |
| 3          | 601.6 | 64.1  | 940    | 8      | US-10-729-830-8      | Sequence 8, Appl      |             |  |  |  |  |  |  |
| 4          | 601.6 | 64.1  | 1691   | 5      | US-10-085-108-8      | Sequence 8, Appl      |             |  |  |  |  |  |  |
| 5          | 601.6 | 64.1  | 1691   | 6      | US-10-160-237-8      | Sequence 8, Appl      |             |  |  |  |  |  |  |
| 6          | 601.6 | 64.1  | 2420   | 5      | US-10-093-766-41     | Sequence 41, Appl     |             |  |  |  |  |  |  |
| 7          | 601.6 | 64.1  | 2420   | 5      | US-10-116-802-250    | Sequence 250, Appl    |             |  |  |  |  |  |  |
| 8          | 601.6 | 64.1  | 2420   | 6      | US-10-117-937-81     | Sequence 81, Appl     |             |  |  |  |  |  |  |
| 9          | 601.6 | 64.1  | 2420   | 8      | US-10-741-466-5      | Sequence 5, Appl      |             |  |  |  |  |  |  |
| 10         | 601.6 | 64.1  | 2420   | 8      | US-10-657-022-81     | Sequence 81, Appl     |             |  |  |  |  |  |  |
| 11         | 601.6 | 64.1  | 2420   | 8      | US-10-807-308-17     | Sequence 17, Appl     |             |  |  |  |  |  |  |
| 12         | 601.6 | 64.1  | 2420   | 8      | US-10-866-484-5      | Sequence 5, Appl      |             |  |  |  |  |  |  |
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| 14         | 601.6 | 64.1  | 2420   | 9      | US-10-871-708-14     | Sequence 14, Appl     |             |  |  |  |  |  |  |
| 15         | 601.6 | 64.1  | 2420   | 10     | US-11-067-064-81     | Sequence 81, Appl     |             |  |  |  |  |  |  |
| 16         | 601.6 | 64.1  | 2420   | 10     | US-11-067-159-81     | Sequence 81, Appl     |             |  |  |  |  |  |  |
| C 17       | 601.6 | 64.1  | 259903 | 9      | US-10-756-149-3550   | Sequence 3550, Appl   |             |  |  |  |  |  |  |
| C 18       | 600.8 | 64.0  | 2408   | 5      | US-10-027-632-111713 | Sequence 111713, Appl |             |  |  |  |  |  |  |
| C 19       | 600.8 | 64.0  | 2408   | 5      | US-10-027-632-111714 | Sequence 111714, Appl |             |  |  |  |  |  |  |
| C 20       | 600.8 | 64.0  | 2408   | 6      | US-10-027-632-111713 | Sequence 111713, Appl |             |  |  |  |  |  |  |
| C 21       | 600.8 | 64.0  | 2408   | 6      | US-10-027-632-111714 | Sequence 111714, Appl |             |  |  |  |  |  |  |
| 22         | 600   | 63.9  | 1722   | 6      | US-10-177-390-17     | Sequence 17, Appl     |             |  |  |  |  |  |  |
| 23         | 597.2 | 63.6  | 930    | 3      | US-09-766-889A-1     | Sequence 1, Appl      |             |  |  |  |  |  |  |

|   |    |       |      |        |    |                     |                   |
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| c | 24 | 597.2 | 63.6 | 1029   | 6  | US-10-029-386-25080 | Sequence 25080, A |
| c | 25 | 594   | 63.3 | 996    | 6  | US-10-029-386-25452 | Sequence 25452, A |
|   | 26 | 522.4 | 55.6 | 1084   | 6  | US-10-267-384-110   | Sequence 110, App |
|   | 27 | 522.4 | 55.6 | 1094   | 6  | US-10-267-384-109   | Sequence 109, App |
|   | 28 | 461   | 49.1 | 1716   | 5  | US-10-093-766-38    | Sequence 38, Appl |
|   | 29 | 461   | 49.1 | 1742   | 5  | US-10-157-031-51    | Sequence 51, Appl |
|   | 30 | 461   | 49.1 | 1744   | 9  | US-10-756-149-74    | Sequence 74, Appl |
|   | 31 | 461   | 49.1 | 1895   | 5  | US-10-102-524-1696  | Sequence 1696, Ap |
|   | 32 | 461   | 49.1 | 1895   | 8  | US-10-482-029-147   | Sequence 147, App |
|   | 33 | 455   | 48.5 | 954    | 7  | US-10-218-095-1     | Sequence 1, Appl  |
|   | 34 | 455   | 48.5 | 961    | 8  | US-10-753-158-49    | Sequence 49, Appl |
|   | 35 | 455   | 48.5 | 1019   | 8  | US-10-723-860-4796  | Sequence 4796, Ap |
|   | 36 | 428.6 | 45.6 | 1956   | 3  | US-09-864-761-4953  | Sequence 4953, Ap |
|   | 37 | 428.6 | 45.6 | 4559   | 6  | US-10-117-937-82    | Sequence 82, Appl |
|   | 38 | 428.6 | 45.6 | 4559   | 8  | US-10-657-022-82    | Sequence 82, Appl |
|   | 39 | 428.6 | 45.6 | 4559   | 10 | US-11-067-064-82    | Sequence 82, Appl |
|   | 40 | 428.6 | 45.6 | 4559   | 10 | US-11-067-159-82    | Sequence 82, Appl |
|   | 41 | 428.6 | 45.6 | 302250 | 3  | US-09-962-832-154   | Sequence 154, App |
| c | 42 | 428.6 | 45.6 | 302250 | 3  | US-09-962-832-154   | Sequence 154, App |
|   | 43 | 428.6 | 45.6 | 302250 | 9  | US-10-843-641A-6040 | Sequence 6040, Ap |
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|   | 45 | 423   | 45.0 | 1375   | 6  | US-10-155-333-2     | Sequence 2, Appl  |

ALIGNMENTS

RESULT 1  
US-10-729-830-10  
; Sequence 10, Application US/10729830  
; Publication No. US20050032730A1  
; GENERAL INFORMATION:  
; APPLICANT: Von der Muelbe, Florian  
; APPLICANT: Heerx, Ingmar  
; APPLICANT: Pascolo, Steve  
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA  
; FILE REFERENCE: 2793-1-001PCT/CIP  
; CURRENT APPLICATION NUMBER: US/10/729,830  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: PCT/EP02/06180  
; PRIOR FILING DATE: 2002-06-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 939  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Description of Artificial Sequence: MAGE1: mRNA  
; FEATURE:  
; OTHER INFORMATION: with increased G/C-content  
; FEATURE:  
; OTHER INFORMATION: Start codon: aug (nucleotides 1 to 3), stop codon:  
; OTHER INFORMATION: uga (nucleotides 937 to 939)  
US-10-729-830-10

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| Query Match               |     |   |     | 100.0%; Score 939; DB 8; Length 939; |  |  |  |
| Best Local Similarity     |     |   |     | 100.0%; Pred. No. 4.7e-217;          |  |  |  |
| Matches 939; Conservative |     |   |     | 0; Mismatches 0; Indels 0; Gaps 0;   |  |  |  |
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| Qy                        | 121 | GGCAGCGUGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG  | 180 |                                      |  |  |  |
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; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CFP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 11
; LENGTH: 939
; TYPE: RNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: with alternative use of codon
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 1 to 3), stop codon:
; OTHER INFORMATION: uga (nucleotides 937 to 939)
US-10-729-830-11

Query Match      85.9%; Score 806.2; DB 8; Length 939;
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Db 361 GAGCGGUCACGAGGCGGAGAGCUGGAGAGCGUCAAAGAAUCAAAGCAUCCUGUUC 420
Qy 421 CCGGAGAUUUCCGCAAGGCGAGCGAGCGCAGCAGCUGGUGUUUCCGCAUCGAGCUAAG 480
Db 421 CCGGAGAUUUCCGCAAGGCGAGCGAGCGCAGCAGCUGGUGUUUCCGCAUCGAGCUAAG 480
Qy 481 GAGCGGAGCAGCGGCGGCGAGCAGCGCGUACGUGUACGUGGCGCUGAGCUAGCAG 540
Db 481 GAGCGGAGCAGCGGCGGCGAGCAGCGCGUACGUGUACGUGGCGCUGAGCUAGCAG 540
Qy 541 GGCUCUGGCGGACAGCAGAUCCGGAAGAGGCGUUCUUGAUCAUCGUUCCUGUG 600
Db 541 GGCUCUGGCGGACAGCAGAUCCGGAAGAGGCGUUCUUGAUCAUCGUUCCUGUG 600
Qy 601 AUGAUCGGAUGGAGGGCGGCCAGCGCGGAGGAGAGAUUCUGGAGGAGCUGAGCGUC 660
Db 601 AUGAUCGGAUGGAGGGCGGCCAGCGCGGAGGAGAGAUUCUGGAGGAGCUGAGCGUC 660
Qy 661 AUGAGGUCUACGACGCGCGGAGCAGCGCGUACGCGGAGCGCGCGGAGCUGCUGACG 720
Db 661 AUGAGGUCUACGACGCGCGGAGCAGCGCGUACGCGGAGCGCGCGGAGCUGCUGACG 720
Qy 721 CAGGACUUGGUCAGGAGAGAUUACUGGAGUACCGCAGGUCUCCGAGCAGCGACCGCGG 780
Db 721 CAGGACUUGGUCAGGAGAGAUUACUGGAGUACCGCAGGUCUCCGAGCAGCGACCGCGG 780
Qy 781 CGCUACGAGUUCUUGUGGGGCCCGCGCGCGGAGAGAGAGCUACGCUAAGGUCUG 840
Db 781 CGCUACGAGUUCUUGUGGGGCCCGCGCGCGGAGAGAGAGCUACGCUAAGGUCUG 840
Qy 841 GAGUACGUAUCAAAGGUCGCGCGGUCUUCUUCUUCUCCGAGCUGCGGAGCGG 900
Db 841 GAGUACGUAUCAAAGGUCGCGCGGUCUUCUUCUUCUCCGAGCUGCGGAGCGG 900
Qy 901 GCGCUGCGGAGGAGGAGGCGGUCUGAGCGUGAUGA 939
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|    |      |  |      |
|----|------|--|------|
| Qy | 301  | GUCAUCACGAAGAAGUUCGCGGACACCGUUGGCUUCCUGUGCUAAGUACCGCGCGC     | 360  |
| Db | 504  | GTAATCACTAAGAAGTGGCTGATTTGGTTGGTTTCTGCTCCTCAATATCGAGCCAGG    | 563  |
| Qy | 361  | GAGCGGUCACGAAGCGGAGAGUUGUGAGAGCGUACUACAAGACUACGACUUC         | 420  |
| Db | 564  | GAGCCAGTCACAAAGGCGAAGAAATGCTGGAGAGTGTATCAAAAATTAACAGCACTGTTT | 623  |
| Qy | 421  | CCGGAGUUCUGCGCAAGCGGAGCGAGCCUGCAGCGUGGUCUUGCGCAUCGACGCUAAG   | 480  |
| Db | 624  | CTGAGATCTTCGGCAAGCCTCTGAGTCTTGCAGCTGGTCTTTGGCATTGACGTGAAG    | 683  |
| Qy | 481  | GAGGCGGACCCGACCGGCGCACAGCUACGUCUGGUCAGUGCGUGGCGUGAGCUACGAC   | 540  |
| Db | 684  | GAAACAGACCCACCGGCCACTCTATGCTCTTGTCTCACTGCTAGGTCTCTCTATGAT    | 743  |
| Qy | 541  | GGCUGUGGCGGACAAACAGAUCAUGCGAAGCGGCUUCUGAUCGACUUCUGUC         | 600  |
| Db | 744  | GGCTGCTGGGTGATAATCAGATCATGCGCAAGCAGGCTTCTGATAATTGCTGCTG      | 803  |
| Qy | 601  | AUGAUCGAGUUGGAGGCGGCGCACCGCGCGAGGAGGAGAUUCUGGAGGAGGUGAGCUC   | 660  |
| Db | 804  | ATGATTGCAATGGAGGCGGCGCATGCTCTGAGGAGGAAATCTGGGAGGAGCTGAGTGT   | 863  |
| Qy | 661  | AUGGAGGUCAACGACGCGCGGAGCACAGCGCUACGCGAGCGCGCAAGCTUGAGC       | 720  |
| Db | 864  | ATGGAGGTGATGATGGAGGAGGAGCAGTGTCTATGGGAGCGCCAGAGCTGCTCACC     | 923  |
| Qy | 721  | CAGGACCUUGGCGGAGGAGAAUACUGGAGUACCGCCAGGUCGCGGACGACGACCGCG    | 780  |
| Db | 924  | CAAGATTTGGTGACGAGAAAGTACCTGGAGTACCGGACAGGTGCGGACAGTGATCCGCA  | 983  |
| Qy | 781  | CGCUACGAGUUCUGUGGGCGCGCGCGCGGCGGAGGAGAGCAGCUACGUAAGUUCUG     | 840  |
| Db | 984  | CGCTATGATTTCTGTGGGTCCAAAGGCGCTCGCTGAAACCAAGCATATGTGAAAGTCTT  | 1043 |
| Qy | 841  | GAGUACGUAACGAGGCGCGCGCGCGCUUCUUCUCCGAGCGGCGGAGCGCGGAGCGG     | 900  |
| Db | 1044 | GAGTATGATCAAGTCACTGTCAGAGAGTTGCTTTTCTTCCCATCCCTGCGGTGAAGCA   | 1103 |
| Qy | 901  | GGCUGCGGAGGAGGAGGCGGCGUUCUGAGCGUGA                           | 936  |
| Db | 1104 | GCTTTGAGAGGAGGAGGAGGAGTCTGAGCATGA                            | 1139 |

RESULT 6  
US-10-093-766-41  
; Sequence 41, Application US/10093766  
; Publication No. US20030013099A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasek, Amy W.  
; APPLICANT: Jones, David A.  
; APPLICANT: Karpf, Adam R.  
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS  
; FILE REFERENCE: PA-0047 US  
; CURRENT APPLICATION NUMBER: US/10/093,766  
; CURRENT FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PERL Program  
; SEQ ID NO 41  
; LENGTH: 2420  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030013099A1 410721.1  
US-10-093-766-41

Query Match 64.1%; Score 601.6; DB 5; Length 2420;  
Best Local Similarity 64.7%; Pred. No. 1.2e-135;  
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

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; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 250
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No: 410721.1
US-10-116-802-250

Query Match      64.1%; Score 601.6; DB 5; Length 2420;
Best Local Similarity 64.7%; Pred. No. 1.2e-135;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

Qy 1 AUGAGCCUGGAGCGGAGCCGACUGCAUGCAAGCCGAGGAGCGCGGAGGCGGCGAG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
626 ATGTCTCTTGAAGAGAGGCTGCTCACTGCAAGCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy 61 GAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
686 GAGGCCCTGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 745

Qy 121 GGCAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
746 GGCACCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 805

Qy 181 GCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
806 GCCTCCGCGCTTCCCACTTACCATCACTTCACTCGACAGAGGCAACCCAGTGAGGTTCC 865

Qy 241 AGCAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
866 AGCAGCGCGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 925

Qy 301 AUGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
926 ATGATCTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 985

Qy 361 GAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
986 GAGCCAGTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1045

Qy 421 CCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1046 CCTGAGATCTTCCGGAAGCCCTCTGAGTCTTGTGAGTGTGTGTGTGTGTGTGTGT 1105

Qy 481 GAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1106 GAAGCAGACCCCAACCGGCCATCTCTATGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 1165

Qy 541 GGCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1166 GGCCTGCTGGGTGATATCAGATCATGCCCCAAGCAGGCTTCTCTGATATAATTTGCTGTCT 1225

Qy 601 AUGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1226 ATGATTCGAATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1285

Qy 661 AUGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1286 ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1345

Qy 721 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1346 CAAGATTTGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1405

Qy 781 CGCUACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1406 CGCTATGAGTTCCTGTGGGTCCTCAAGGGCCCTCGCTGAAACACGAGCTATGTGAAGTCCT 1465

Qy 841 GAGUACGUAUACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1466 GAGTATGTATCAAGGTGAGTCAAGAGTTCGCTTTTCTTCCATCCCTCGTGAAGCA 1525

Qy 901 GCGCUGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 936
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1526 GCTTTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1561

RESULT 8
US-10-117-937-81
; Sequence 81, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-117-937-81

Query Match      64.1%; Score 601.6; DB 6; Length 2420;
Best Local Similarity 64.7%; Pred. No. 1.2e-135;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

Qy 1 AUGAGCCUGGAGCGGAGCCGACUGCAUGCAAGCCGAGGAGCGCGGAGGCGGCGAG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
626 ATGTCTCTTGAAGAGAGGAGTCTGCACTGCAAGCTGAGGAAGCCCTTGAGGCCCAACAA 685

Qy 61 GAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
686 GAGGCCCTGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 745

Qy 121 GGCAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
746 GGCACCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 805

Qy 181 GCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
806 GCCTCCGCGCTTCCCACTTACCATCACTTCACTCGACAGAGGCAACCCAGTGAGGTTCC 865

Qy 241 AGCAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
866 AGCAGCGCGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 925

Qy 301 AUGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
926 ATGATCTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 985

Qy 361 GAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
986 GAGCCAGTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1045

Qy 421 CCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1046 CCTGAGATCTTCCGGAAGCCCTCTGAGTCTTGTGAGTGTGTGTGTGTGTGTGTGT 1105

Qy 481 GAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1106 GAAGCAGACCCCAACCGGCCATCTCTATGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 1165

Qy 541 GGCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1166 GGCCTGCTGGGTGATATCAGATCATGCCCCAAGCAGGCTTCTCTGATATAATTTGCTGTCT 1225

Qy 601 AUGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1226 ATGATTCGAATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1285

Qy 661 AUGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1286 ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1345

Qy 721 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1346 CAAGATTTGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1405

Qy 781 CGCUACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1406 CGCTATGAGTTCCTGTGGGTCCTCAAGGGCCCTCGCTGAAACACGAGCTATGTGAAGTCCT 1465
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Db 866 AGCAGCCGTGAAGAGGAGGGGCCCAAGCACCTCTTGTATCTCTGGAGTCTTGTTCGGAGCA 925  
Qy 301 GUCAUACGAGAAAGGUCGCGAGACCUUGUCGGUCCUUGUCUGAAGUACCGCGCGC 360  
Db 926 GTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTCTGCTCCTCAATATCGAGCCAGG 985  
Qy 361 GAGCCGUCACGAAGGCGGAGAGUUGUGGAGAGCGUCAUCAAGAAACUAACAGCACUGCUUC 420  
Db 986 GAGCCAGTCAAAAGGCGAAGATCTGAGAGTGTATCAAAAATTACAAGCACTGTGTTT 1045  
Qy 421 CCGGAGAUUUCGCAAGGCGAGCGAGAGCCUGCAGCGUGUCUGGCAUCGAGCUAAG 480  
Db 1046 CCTGAGATCTTCGGCAAGCCTCTGAGTCTTGCAGCTGGTCTTTGGCAITGACGTGAAG 1105  
Qy 481 GAGCGGACCCGACGCGGCCACAGCUAGUCCUGGUCAGUGCCUGGCGCUGAGCUAGCAC 540  
Db 1106 GAAGCAGACCCACCGGCCACTCTATGTCTTGTCACTGCTAGGTCTCTCTATGAT 1165  
Qy 541 GGCUGUGGCGGCAACACGAUCAUGCCGAAGACGGGCUUCCUGAUAUCGUCUGUC 600  
Db 1166 GGCCTGCTGGGTGATAATCAGATCATGCCCCAAGACAGGCTTCTGATAAATTGTCTGGTC 1225  
Qy 601 AUGAUCGAGUGAGGCGGCCACGCGCGGAGGAGGAGUUCUGGAGGAGCUGAGGUC 660  
Db 1226 ATGATTGCAATGGAGGGCGGCCATGCTCTGAGGAGGAATCTGGGAGGAGCTGAGTGTG 1285  
Qy 661 AUGAGGUCUACGACGCGCGGAGCACAGCGCGUACGCGGAGCGCCGAGCUGCUGACG 720  
Db 1286 ATGGAGGTGATATGGAGGGAGGACAGTGCCTATGGGAGCCAGGAGCTCTCACC 1345  
Qy 721 CAGGACUGGUCGAGGAGAAAGUACUGGAGUACCGCAGGUCUCCGCGACAGCGCGG 780  
Db 1346 CAAGATTGGTGCAGGAAAGTACCTGGAGTACCGGAGGTCGCGGACAGTGTCCGCA 1405  
Qy 781 CGCUACGUAUUCUGGGGCGCGCGCGGCGGAGGAGGAGCAGCUAGGUCUG 840  
Db 1406 CGCTATGAGTTCTGTGGGGTCCAAAGGGCCCTCGCTGAACACAGCTATGTGAAAGTCTTT 1465  
Qy 841 GAGUACGUAUACGAGGAGGAGGCGCGCGGCGUCCUUCUCCGAGCGCUGCGGAGCGG 900  
Db 1466 GAGTATGTGATCAGGTTCAGTGCAGAGTTCGCTTTTCTTCCATCCCTGCGTGAAGCA 1525  
Qy 901 GCGCUGCGCGAGGAGGAGGCGGCGUUCUGAGCGUGA 936  
Db 1526 GCTTTGAGAGGAGGAGGAGGAGGAGTCTGAGCATGA 1561

RESULT 2  
US-11-178-134-6  
; Sequence 6, Application US/11178134  
; Publication No. US20060019290A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Pittsburgh - of The Commonwealth System of  
; APPLICANT: Higher Education  
; APPLICANT: Godfrey, Tony  
; APPLICANT: Hughes, Steven  
; APPLICANT: Xi, Liqiang  
; APPLICANT: Gooding, William E  
; APPLICANT: Raja, Siva E  
; TITLE OF INVENTION: Identification of Markers in Esophageal Cancer, Colon Cancer,  
; FILE OF INVENTION: Head and Neck Cancer and Melanoma  
; FILE REFERENCE: 030160  
; CURRENT APPLICATION NUMBER: US/11/178,134  
; CURRENT FILING DATE: 2005-07-08  
; PRIOR APPLICATION NUMBER: 60/586,599  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: 60/587,019  
; PRIOR FILING DATE: 2004-07-09  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 1722

; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-178-134-6  
Query Match 63.9%; Score 600; DB 12; Length 1722;  
Best Local Similarity 64.6%; Pred. No. 6.3e-121;  
Matches 605; Conservative 121; Mismatches 210; Indels 0; Gaps 0;  
Qy 1 AUGAGCCUGAGCAGCGCAGCUGCAGCAACGCCGAGAGGAGGCGGCGGAGGCGCAGCAG 60  
Db 188 ATGCTCTTTCGAGCAGAGGAGTCTGCACCTGCAAGCCTGAGGAAGCCCTTGAAGCCCAAA 247  
Qy 61 GAGCGCUGGCGCUGGUCUGCAGGGCGGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCUG 120  
Db 248 GAGGCCCTGGGCTGTGTGTGTCAGGCTGCGCCTCTCTCTCTCTCTCTCTCTCTCTCT 307  
Qy 121 GGCACTGUGAGGAGGUCGCCGAGCGGGGCGAGCACCGGCCGCGAGAGCCCGCAGGGC 180  
Db 308 GGCACTCTGAGAGGAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 367  
Qy 181 GCGAGCGGCUUCCGCGAGCAGCAACUUCACGCGCGCAGCGCCAGCGCGAGGCGGAGC 240  
Db 368 GCCTCGGCTTTCCTCACTACCATCACTCTGAGAGGCAACCCAGTGAAGGTTTC 427  
Qy 241 AGCAGCGCGAGGAGGAGGCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 300  
Db 428 AGCAGCGGTGAAGAGGAGGCGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 487  
Qy 301 GUCAUACGAAGAAGGUCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 360  
Db 488 GTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTCTGCTCTCTCAAAATACGAGCC 547  
Qy 361 GAGCGGUCACGAAGGCGGAGUUGUGGAGGAGCGUACUAAAGAACUACAAAGCAGCAG 420  
Db 548 GAGCCAGTCAAAAGGCGAAGATGCTGAGAGTGTCTATCAAAAATTACAAGCACTGT 607  
Qy 421 CCGGAGUUCUCCGAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480  
Db 608 CCTGAGATCTTCGGCAAGCCTCTGAGTCTTGGAGCTGTCTTGGCATTTGAGTGAAG 667  
Qy 481 GAGCGGACCCGAGCGGCGCACAGCUACGUCUCCGUCACGUGGCGGCGGCGGCGGAG 540  
Db 668 GAAGCAGACCCACCGGCGACTCTATGTCTCTTGTACCTGCTCTCTCTCTCTCTCT 727  
Qy 541 GCGCUGCGGCGAGCAACACAGAUUCCGAAAGCGGCGUUCUUGAUAUCGUCUCCUG 600  
Db 728 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCTCTGATAATTGCTG 787  
Qy 601 AUGAUCGAGGAGGCGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
Db 788 ATGATTGCAATGGAGGCGGCGCATGCTCTGAGAGGAGGAATCTGGGAGGAGCTGAG 847  
Qy 661 AUGAGGUCUACGACGCGCGCGAGCAGCAGCGCGUACGCGGAGCGCGCGCAAGCUG 720  
Db 848 ATGGAGGTGTATGATGGGAGGAGCAGTGCCTATGCGGAGCGCCAGAGCTCTCACC 907  
Qy 721 CAGGACUGGUCGAGGAGAAAGUACCUUGAGUACCGCAGGUCUCCGCGAGCAGGAG 780  
Db 908 CAAGATTGGTGCAGGAAAGTACCTGAGATACCGGAGGAGGAGGAGGAGGAGGAGG 967  
Qy 781 GCUACGUAUCCUGUGGGCGCGCGCGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGC 840  
Db 968 CGCTATGAGTTCTGTGGGGTCCAAAGGGCCCTTGTCTGAAACCACTATGTGAAAGT 1027  
Qy 841 GAGUACGUAUACGAGGUCAGCGCGCGGCGGCGGCGUUCUUCUCCGAGCGGCGGAG 900  
Db 1028 GAGTATGTGATCAAGGTTCAGTGCAGAGTTCGCTTTTCTTTCTTCTTCTTCTTCT 1087  
Qy 901 GCGCUGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 936  
Db 1088 GCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1123



Qy 220 CGCCAGCCGAGCGAGCGAGCGAGCGCGCGAGAGAGGCGCCCGAGCACAGCUGCAUC 279  
| | | | |  
Db 450 AGCCAATCCTATGAGGATCTCAGCAACCAAGAGAGAGGCGCCCAAGACCTTCCCTGCAC 509  
| | | | |  
Qy 280 CUGAGAGCCUGUUCGCGCGGUAUCACAGAGAGAGGUCGCGGACCGUUGCGUUCUG 339  
| | | | |  
Db 510 CTGAGTCCGAGTTCCAGCAGCACTCAGTAGGAAGGTGGCCGAGTTGGTTCATTTCTG 569  
| | | | |  
Qy 340 CUGCUGAAGUACCGCGCGCGAGCGCGGUAUCAGAGGCGAGAGUUGCUGGAGCGGUAUC 399  
| | | | |  
Db 570 CTCCTCAAGTATCAGCAGGAGCGGTCAAGGCGAGAAATGCTGGGAGTGTCTG 629  
| | | | |  
Qy 400 AAGAAUACAGCAUGUUCGCGAGAUUCUUGGCAAGGCGAGAGCGAGCUGCAGCUG 459  
| | | | |  
Db 630 GGAATATGGCAGTATTTCTTCTGTGATCTTCAAGCAAGCTTCCAGTTCTTTCAGCTG 689  
| | | | |  
Qy 460 GUCUUGCGCAGCAGCUGCAGGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 519  
| | | | |  
Db 690 GTCTTTGGCATCGAGCTGATGGAAGTGAGACCCCATCGGCCACTTGTATCATCTTTGCCACC 749  
| | | | |  
Qy 520 UGCCUGGCGCGAGCAGCGCGCGUGCUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 579  
| | | | |  
Db 750 TGCCTGGGCTCTCTACGATGGCTGCTGGGTGACATCAGATCATGCCCCAAGCGCAGC 809  
| | | | |  
Qy 580 UUCUGAUCUUGCUGGUAUGAUCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAG 639  
| | | | |  
Db 810 CTCCTGATATCTGCTGGCATAATCGCAAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 869  
| | | | |  
Qy 640 AUCUGGAGGAGCAGGUAUGGAGGUAUCAGCAGCGCGCGGCGGCGGCGGCGGCGGCGG 699  
| | | | |  
Db 870 ATCTGGGAGGAGCTGAGTGTGTAGAGGTGTTGAGGCGGAGGAGACAGTATCTTGGGG 929  
| | | | |  
Qy 700 GAGCGCGCGAAGCAGCAGGACCGUGCUGCAGGAGAGUACCGGAGUACCGGCGAG 759  
| | | | |  
Db 930 GATCCCAAGAGCTGCTCACCCACATTTCTGCGAGGAACTACTTGGAGTACCGGCGAG 989  
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Qy 760 GUCCCCGAGCAGCAGCGCGCGGUAUGUUGUUGGCGGCGGCGGCGGCGGCGGCGGCGGAG 819  
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Db 990 GTCCCGGCGAGTATCTGCTGATTTATGAATTTCTGTGGGTCCCAAGGCGGCGGCGGCGG 1049  
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Qy 820 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 879  
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Db 1050 ACCAGCTATGTGAAGTCTGCACCATATGTTAAAGATCAGTGAGGACCTCATTTC 1109  
| | | | |  
Qy 880 UUCGCGAGCUGCGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 936  
| | | | |  
Db 1110 TACCACCCCTGCATGAGTGGGTTTGAGAGAGGCGGAGAGTGTGAGTCTGAGCAGGA 1166  
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RESULT 5  
US-11-155-288-26  
; Sequence 26, Application US/11155288  
; Publication No. US20060008468A1  
; GENERAL INFORMATION:  
; APPLICANT: Chiang, Chih-Sheng  
; APPLICANT: Simard, John J.L.  
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED  
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS  
; FILE REFERENCE: MANK.050A  
; CURRENT APPLICATION NUMBER: US/11/155,288  
; PRIOR FILING DATE: 2005-06-17  
; PRIOR APPLICATION NUMBER: 60/580,969  
; PRIOR FILING DATE: 2004-06-17  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 4204  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-155-288-26

Query Match 44.0%; Score 413.4; DB 12; Length 4204;

Best Local Similarity 55.8%; Pred. No. 1.2e-80;  
Matches 534; Conservative 101; Mismatches 301; Indels 21; Gaps 2;  
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Qy 61 GAGCGCGGCGCUGGUCUGCUGCAGGCGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAG 111  
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Db 2525 GAGCGCGGCGCUGGUCUGCUGCAGGCGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2584  
| | | | |  
Qy 112 -----CUGGUCUGGCGCAGCUGGAGGAGGUCGCGGCGGCGGCGGCGGCGGCGG 159  
| | | | |  
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| | | | |  
Qy 160 CCGCGCAGAGCCGCGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 219  
| | | | |  
Db 2645 CTTCCCGAGAGTCTCAGGAGGCTCCAGGCTCCCACTACCATGAACCTACCTCTCTGG 2704  
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Qy 220 CGCAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 279  
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Db 2705 AGCCAATCTTATGAGGACTCCAGCAACCAAGAGAGGAGGCGGCGGCGGCGGCGGCGG 2764  
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Db 2765 CTGGAGTCCGAGTTCAGAGCAGCAGTCTGAGGAGGAGGCGGCGGCGGCGGCGGCGGCGG 2824  
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Qy 340 CUCGUAAGUACCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 399  
| | | | |  
Db 2825 CTCCTCAAGTATCAGCGCAGGAGCGGTCACAAAGGCGAGAAATGTGGGAGTGTCTGTC 2884  
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Qy 400 AAGAAUACAGCAUGUUCGCGGAGUUCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 459  
| | | | |  
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Qy 460 GUCUUGCGCAGCAGCAGCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 519  
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Db 2945 GTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCGGCGGCGGCGGCGGCGGCGG 3004  
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Qy 580 UUCUGAUCUUGCUGGUAUGAUCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAG 639  
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Db 3065 CTCCTGATATCTGCTGGCATAATCGCAAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 3124  
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Qy 700 GAGCGCGCAGCAGCAGCAGCAGGAGCUGGUCAGGAGAGUACCGGAGUACCGGCGAG 759  
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Qy 880 UUCGCGAGCUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 936  
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Db 3365 TACCACCCCTGCATGAGTGGGTTTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3421  
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RESULT 6  
US-09-925-065A-859557/c  
; Sequence 859557, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:

















GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:02:13 ; Search time 190.385 Seconds  
(without alignments)  
8767.110 Million cell updates/sec

Title: US-10-729-830-11

Perfect score: 939

Sequence: 1 augagccugagcgagcgagcag.....aggcgugagcgccugauga 939

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA.\*
- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*
  - 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*
  - 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
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  - 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 641.6 | 68.3        | 1624   | 3     | US-09-392-714-18    |
| 2          | 641.6 | 68.3        | 1624   | 3     | US-09-949-016-703   |
| 3          | 641.6 | 68.3        | 1624   | 3     | US-09-949-016-2688  |
| 4          | 641.6 | 68.3        | 1691   | 2     | US-08-993-118-8     |
| 5          | 641.6 | 68.3        | 1691   | 3     | US-08-845-528C-8    |
| 6          | 641.6 | 68.3        | 1691   | 3     | US-09-066-281B-8    |
| 7          | 641.6 | 68.3        | 1691   | 3     | US-09-468-433C-8    |
| 8          | 641.6 | 68.3        | 2420   | 2     | US-08-465-167A-23   |
| 9          | 641.6 | 68.3        | 2420   | 3     | US-08-056-105-4     |
| 10         | 641.6 | 68.3        | 2420   | 3     | US-08-627-820-23    |
| 11         | 641.6 | 68.3        | 5699   | 3     | US-09-949-016-12445 |
| 12         | 641.6 | 68.3        | 5699   | 3     | US-09-949-016-14430 |
| 13         | 629.6 | 67.1        | 2419   | 2     | US-07-807-043B-7    |
| 14         | 629.6 | 67.1        | 2419   | 2     | US-08-299-849B-7    |
| 15         | 629.6 | 67.1        | 2419   | 2     | US-08-142-368A-7    |
| 16         | 629.6 | 67.1        | 2419   | 3     | US-08-967-727-7     |
| 17         | 629.6 | 67.1        | 2419   | 3     | US-08-037-230D-7    |
| 18         | 629.6 | 67.1        | 2419   | 3     | US-09-583-850-7     |
| 19         | 629.6 | 67.1        | 2419   | 3     | US-09-579-197-7     |
| 20         | 629.6 | 67.1        | 2419   | 3     | US-09-404-026-7     |
| 21         | 629.6 | 67.1        | 2419   | 3     | US-09-312-464-7     |
| 22         | 629.6 | 67.1        | 2419   | 3     | US-09-583-848A-7    |
| 23         | 629.6 | 67.1        | 5674   | 2     | US-07-807-043B-8    |
| 24         | 629.6 | 67.1        | 5674   | 2     | US-08-190-411A-1    |

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|----|-------|------|------|---|-------------------|-------------------|
| 25 | 629.6 | 67.1 | 5674 | 2 | US-08-299-849B-8  | Sequence 8, Appli |
| 26 | 629.6 | 67.1 | 5674 | 2 | US-08-560-024-1   | Sequence 1, Appli |
| 27 | 629.6 | 67.1 | 5674 | 2 | US-08-142-368A-8  | Sequence 8, Appli |
| 28 | 629.6 | 67.1 | 5674 | 3 | US-08-967-727-8   | Sequence 8, Appli |
| 29 | 629.6 | 67.1 | 5674 | 3 | US-08-037-230D-8  | Sequence 8, Appli |
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| 31 | 629.6 | 67.1 | 5674 | 3 | US-09-579-197-8   | Sequence 8, Appli |
| 32 | 629.6 | 67.1 | 5674 | 3 | US-09-404-026-8   | Sequence 8, Appli |
| 33 | 629.6 | 67.1 | 5674 | 3 | US-09-312-464-8   | Sequence 8, Appli |
| 34 | 629.6 | 67.1 | 5674 | 3 | US-09-583-848A-8  | Sequence 8, Appli |
| 35 | 565.6 | 60.2 | 1084 | 2 | US-08-184-009-110 | Sequence 110, App |
| 36 | 565.6 | 60.2 | 1084 | 2 | US-08-458-356-110 | Sequence 110, App |
| 37 | 565.6 | 60.2 | 1084 | 3 | US-08-460-736-110 | Sequence 110, App |
| 38 | 565.6 | 60.2 | 1084 | 3 | US-09-535-370-110 | Sequence 110, App |
| 39 | 565.6 | 60.2 | 1084 | 3 | US-09-663-667-110 | Sequence 109, App |
| 40 | 565.6 | 60.2 | 1094 | 2 | US-08-184-009-109 | Sequence 109, App |
| 41 | 565.6 | 60.2 | 1094 | 2 | US-08-458-356-109 | Sequence 109, App |
| 42 | 565.6 | 60.2 | 1094 | 3 | US-08-460-736-109 | Sequence 109, App |
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| 44 | 565.6 | 60.2 | 1094 | 3 | US-09-663-667-109 | Sequence 109, App |
| 45 | 491.6 | 52.4 | 1022 | 3 | US-09-056-105-8   | Sequence 8, Appli |

ALIGNMENTS

RESULT 1

US-09-392-714-18  
; Sequence 18, Application US/09392714A  
; Patent No. 6686147  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Matthew J.  
; APPLICANT: Gure, Ali O.  
; APPLICANT: Williamson, Barbara  
; APPLICANT: Chen, Yao-Tseng  
; APPLICANT: Old, Lloyd J.  
; TITLE OF INVENTION: Cancer Associated Antigens and Uses  
; FILE REFERENCE: L0461/7062  
; CURRENT APPLICATION NUMBER: US/09/392,714A  
; CURRENT FILING DATE: 1999-09-09  
; EARLIER APPLICATION NUMBER: PCT/US98/14679  
; EARLIER FILING DATE: 1998-07-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 18  
; LENGTH: 1624  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-392-714-18

|                       |       |  |          |            |      |        |       |
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| Query Match           | 58.3% | Score  | 641.6;   | DB         | 3;   | Length | 1624; |
| Best Local Similarity | 67.4% | Pred. No.  | 6.5e-95; |            |      |        |       |
| Matches               | 631;  | Conservative   | 121;     | Mismatches | 184; | Indels | 0;    |
| Gaps                  | 0;    |  |          |            |      |        |       |
| Qy                    | 1     | AUGAGCCUGAGGAGCGCAGCCUGCAGCAAGCCGAGGAGCCUGGAGGCCAGCAG        | 60       |            |      |        |       |
| Db                    | 139   | ATGTCTTTGAGCAGAGGAGTCTGCACTGAGAGGCTTGAGGCCCTTGAGGCCCAACAA    | 198      |            |      |        |       |
| Qy                    | 61    | GAGGCCUGGCGCCUGGUGUGCGUGCAGCGCCGCCACACAGCAGCAGCCCGCCUGGUGUG  | 120      |            |      |        |       |
| Db                    | 199   | GAGGCCCTGGGCGCTGGTGTGTGTGAGGCTGCCACCTCTCTCTCTCTCTCTCTCTCTG   | 258      |            |      |        |       |
| Qy                    | 121   | GGCAGCCUGAGGAGGUGCCCGCCGCGCAGCAGCCCGCCCGCCAGAGCCCGCCAGAGGC   | 180      |            |      |        |       |
| Db                    | 259   | GGCAGCCCTGGAGGAGGTGCCCACTGTGGGTGAACAGATCTCTCCAGAGTCTCTCAGGGA | 318      |            |      |        |       |
| Qy                    | 181   | GCCAGCCCTUCCCGACCAUCCACUCCCGCCGAGCCAGCCCGCCAGGAGGAGCAGC      | 240      |            |      |        |       |
| Db                    | 319   | GCCTCCGCTTTTCCCACTACATCACTTCTCTGACAGAGGCAACCCAGTGAGGGTTCC    | 378      |            |      |        |       |
| Qy                    | 241   | AGCAGCCGCGAGGAGGAGGCCCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC   | 300      |            |      |        |       |

Db 379 AGCAGCGTGAAGAGGGGCGCCAGCACCTCTTGATATCTGGAGTCTTGTTCGAGCA 438  
Qy 301 GUGAUCACCAAGAGGUGGCGGACCGUGGUGGCUUCUGUGUGUGAUAUACCGCGCCGC 360  
Db 439 GTAATCACTAAGAGGTGGCTGATTGTTGGTTTCTGTCTCTCAATATCGAGCCAGG 498  
Qy 361 GAGCCGUGACCAAGGCGGAGAGUGUGGAGGCGUGAUAUAAGAACUAACAAGCAGCUGCU 420  
Db 499 GAGCCAGTCAAAAGGAGGAGAAATGCTGGAGAGTGTATCAAAAATTAACAAGCACTGTTT 558  
Qy 421 CCCGAGAUUCGCGAAGGCGAGCGAGGUGUGUGUGUGUGUGUGUGUGUGUGUGUGAAG 480  
Db 559 CTTGAGATCTTCGCAAGGCTCTGAGTCTTGAGCTGGTCTTGGCATGAGTGAAG 618  
Qy 481 GAGCCGACCCCGCCAGCAGCUAGCUGUGUGACCGUGUGUGUGUGUGUGUGUGUGUGUG 540  
Db 619 GAAGCAGACCCCGCCAGCTCTATGCTCTGTGACCTGCTAGTCTCTCTATGAT 678  
Qy 541 GCGCUGUGGCGGAGCAACAGAUCAUAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
Db 679 GGCCTGCTGGGTGATATCAATCAATCATGCCAAGACAGGCTTCTGTGATAATTGCTGGTC 738  
Qy 601 AUGAUCGCGAGGAGGCGGCGAGCGCCCGAGGAGGAGAUUCUGGAGGAGGAGGAGGAGG 660  
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Qy 661 AUGAGGUGUACGACGCGCGGAGCAGACGCGCUACGCGGAGGCGCCCGCAGCUGUGAC 720  
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RESULT 2  
US-09-949-016-703  
; Sequence 703, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 703  
; LENGTH: 1624  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-703  
Query Match 68.3%; Score 641.6; DB 3; Length 1624;

Best Local Similarity 67.4%; Pred. No. 6.5e-95;  
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;  
Qy 1 AUGAGCCUGGAGCAGCGCAGCCUGACUCAGAACCGAGAGGCGCCUGAGGCGCCAGCAG 60  
Db 139 ATGTCTCTTTGAGCAGAGGAGTCTGCACCTCAAGCCTTGAGGAGCCCTTGAGGCGCA 198  
Qy 61 GAGGCCUGGCGCUGUGUGUGGAGGCGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGC 120  
Db 199 GAGGCCCTGGCTGTGTGTGAGGCTGCGCACCTCTCTCTCTCTCTCTCTCTCTCTCT 258  
Qy 121 GGCACCTUGGAGGAGGUGCCACCGCGGAGCAGCACCGACCCCGCAGAGCCCGCAGG 180  
Db 259 GGCACCTUGGAGGAGGUGCCACCGCGGAGCAGCACCGACCCCGCAGAGCCCGCAGG 318  
Qy 181 GCGAGCGCCUUCGCCACCAUACCUACCGCGCAGCGCCAGCGCCAGCGAGGCGAGC 240  
Db 319 GCCTCGGCTTCCCACTACCATCACTTCACTCGACAGAGGCAACCCAGTGAGGGTTC 378  
Qy 241 AGCAGCGGAGGAGGAGGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 300  
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Db 439 GTAACTCACTAAGAGGTGGCTGATTGGTTGGTTTCTGTCTCTCAATATCGAGCAG 498  
Qy 361 GAGCCGUGAUCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
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Db 559 CTTGAGATCTTCCGCAAGGCGCTCTGAGTCTTGCAGCTGGTCTTGGCATGAGTGAAG 618  
Qy 481 GAGCCGACCCCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 540  
Db 619 GAAGCAGACCCCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 678  
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Db 679 GGCCTGCTGGGTGATAATCAGATCATGCGCCAGAGAGGCTTCTCTGATAATTGCTG 738  
Qy 601 AUGAUCGCGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
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Qy 661 AUGAGGUGUACGACGCGCGGAGCAGCGCGCUACGCGGAGGCGCCCGCAGCUGUGAC 720  
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Db 919 CGCTATGAGTTCCTGTGGGTGCGAAGGCGCTCTGAGGAGGAGGAGGAGGAGGAGGAG 978  
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Qy 901 GCCCUGCGGAGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 936  
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RESULT 3  
US-09-949-016-2688  
; Sequence 2688, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:



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Db 564 GAGCCAGTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 623
Qy 421 CCCGAGAUUCCGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
Db 624 CCTGAGATCTCGGCAAGCCTCTGAGTCTTGTGATCTTGTGATCTTGTGATCTTGTGAT 683
Qy 481 GAGCCGACCCACCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 540
Db 684 GAAGCAGACCCACCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 743
Qy 541 GGCUGUGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 600
Db 744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGAGAGGCTTCTGATAATTTGCTCTGTC 803
Qy 601 AUGAUCGCAUGAGGAGGCGGCGCAGCGCCCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 804 ATGATTGATGAGGAGGCGGCGCAGCGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 863
Qy 661 AUGAGGUGUACGAGCGCGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 720
Db 864 ATGGAGGTGATGATGGAGGAGGAGCAGTGCCTATGGGAGCGCCAGGAGCTGCTCACC 923
Qy 721 CAGGACUUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Db 924 CAAGATTGGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 983
Qy 781 CGCUACAGAUUCCUGUGGGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db 984 CGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCGCTGAAACAGCTATGTGAAGTCTCTT 1043
Qy 841 GAGUACGUGAUAAGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTCCATCCTCGTGAAGCA 1103
Qy 901 GCCUGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 936
Db 1104 GCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1139
```

## RESULT 5

US-08-845-528C-8

; Sequence 8, Application US/08845528C

; Patent No. 6027924

; GENERAL INFORMATION:

; APPLICANT: LUCAS, Sophie;

; APPLICANT: DE SMET, Charles;

; APPLICANT: BOON-FALLEUR, Thierry

; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR

; TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe &amp; Lynch

; STREET: 805 Third Avenue

```
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,528C
; FILING DATE: April 25, 1997
; CLASSIFICATION: 4335
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5455
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleotides
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; US-08-845-528C-8
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Query Match 68.3%; Score 641.6; DB 3; Length 1691;

Best Local Similarity 67.4%; Pred. No. 6.5e-95;

Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

Qy 1 AUGAGCCUGAGCAGCGCAGCCUGCAGCAAGCCCGAGAGGCGCCUGGAGGCCAGCAG 60

Db 204 ATGCTCTTGAGAGGAGTCTGCACCTGCAAGCTTGAGGAGCCCTTGAGGCCCAAA 263

Qy 61 GAGGCCUGGCGCCUGGUGCGAGCGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGC 120

Db 264 GAGGCCCTGGGCTGT 323

Qy 121 GGCAACCCUGAGGAGGUGCCCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGG 180

Db 324 GGCAACCTGAGAGGAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 383

Qy 181 GCCAGCGCCUUCGCCACCAUACUACCCCGCAGCGCCAGCCAGCCAGCGAGGGCAGC 240

Db 384 GCCTCGGCTTCCCACTTACCTACCTCACTCGACAGAGCAACCCAGTGAGGGTTC 443

Qy 241 AGCAGCGCGAGGAGGAGGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 300

Db 444 AGCAGCGGTGAAGAGGAGGAGGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 503

Qy 301 GUGAUCACCAAGAGGUGGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 360

Db 504 GTAATCACTAAGAGGAGGCGCTGATTTGGTTGGTTTCTGTCTCTCAAAATATGAG 563

Qy 361 GAGCCCGUGACCAAGCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 420

Db 564 GAGCCAGTCAAAAGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 623

Qy 421 CCCGAGAUUCCGCGAGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480

Db 624 CCTGAGATCTTCGGCAAGGCTCTGAGTCTCTGAGTCTCTGAGTCTCTGAGTCTCT 683

Qy 481 GAGGCCAGCCCGCGCCACAGCUACGUGCUGGUGAGCAGCAGCAGCAGCAGCAGCAGC 540

Db 684 GAAGCAGACCCCGCGCCACTCTTGTGTCTTGTGTCTTGTGTCTTGTGTCTTGTGTCT 743

Qy 541 GGCUGUGGCGGAGCAACACGAGCAUCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600

Db 744 GGCCTGTGGGTGATAATCAGATCATGCCCAAGCAGGCTTCTGTGATAATTTGCTCTG 803

Qy 601 AUGAUGCCCAUGGAGGCGCGCCAGCGCCCGCGGAGGAGGAGGAGGAGGAGGAGGAG 660

Db 804 ATGATTGCAATGGAGGCGCCATGCTCTCTGAGGAGGAAATCTGGAGAGCTGAGTGTG 863  
Qy 661 AUGGAGGUGUACGACGCGCGGAGGACACAGCGCCUACGCGAGCCCGCAAGCUGUGUAC 720  
Db 864 ATGGAGGTGTATGATGGGAGGAGGACAGTGCCTATATGGGAGCCGAGGAAGCTGCTACC 923  
Qy 721 CAGGACCUUGUGCAGGAGAAUACCUUGAGUACCGCCAGGUGCCGACAGCGACCCGCG 780  
Db 924 CAAGATTTGGTGACGAAAGTACTCTGAGTACCGGACAGGTGCGGACAGTATCCCGCA 983  
Qy 781 GCUACGAGUUCUGUGGGGCCCCCGCCUGGCGGAGACGACUACUGAAGUGUGUG 840  
Db 984 CGCTATGATGTTCTGTGGGTCCAAAGGCGCTGCTGAAACGAGCTATGTGAAAGTCTT 1043  
Qy 841 GAGUACGUGAUCAGGUGAGCGCCGCGUGGCGUUCUUCGCCAGCGUGCGGAGGCC 900  
Db 1044 GAGTATGTGATCAAGGTCAAGTGCAGAGAGTTCGCTTTTCTTCCATCCCTCGTGAAGCA 1103  
Qy 901 GCCUGCGGAGGAGGCGGCGUGUGAGCCUGA 936  
Db 1104 GCTTTGAGAGGAGGAGGAGGAGTCTGAGCATGA 1139

RESULT 6  
US-09-066-281B-8  
; Sequence 8, Application US/09066281B  
; Patent No. 6475783  
; GENERAL INFORMATION:  
; APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING  
; TITLE OF INVENTION: FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Fulbright & Jaworski L.L.P.  
; STREET: 666 Fifth Avenue  
; CITY: New York City  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/066,281B  
; FILING DATE: April 24, 1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/845,528  
; FILING DATE: April 25, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mary Anne Schofield  
; REGISTRATION NUMBER: 36,669  
; REFERENCE/DOCKET NUMBER: LUD 5455.2 US - JEL/MAS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 318-3100  
; TELEFAX: (212) 752-5958  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1691 base pairs  
; TYPE: nucleotides  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear

US-09-066-281B-8  
Query Match 68.3%; Score 641.6; DB 3; Length 1691;  
Best Local Similarity 67.4%; Pred. No. 6.5e-95;  
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;  
Qy 1 AUGAGCCUGGAGCGGACGCGACGUGCACUGCAAGCCGAGGAGGCCCTUGGAGGCCGACGAG 60

Db 204 ATGTCTCTTGAGCAGAGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACA 263  
Qy 61 GAGGCCUGGCGCCUGGUGUGGAGGCGCGCCACAGCAGCAGCAGCAGCAGCAGCAGCAGC 120  
Db 264 GAGGCCCTTGCGCTGGTGTGTGTGAGGCTGCGCACCTCTCTCTCTCTCTCTCTCTCT 323  
Qy 121 GGCACCCUGGAGGAGGUGCCACCGCGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 180  
Db 324 GGCACCTGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCAGAGTCTCTCAGGA 383  
Qy 181 GCCAGCGCCUUCGCCACCAUCAUCUACCCGCGCAGCGCCAGCAGCAGCAGCAGCAGC 240  
Db 384 GCCTCCGCTTCCCACTACCATCACTTCACTCGACAGAGGCAACCCAGTAGGGTTC 443  
Qy 241 AGCAGCGCGAGGAGGAGGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 300  
Db 444 AGCAGCGGTGAAGAGGAGGCGCCAAAGCACCTCTTGTATCTCTGGAGTCTTGTTC 503  
Qy 301 GUGAUCACCAAGAGGUGCGCGACCGUGGUGGCUUCUGUGUGUAGUAGUAGUAGUAG 360  
Db 504 GTATCACTAAGAGGTGGCTGATTGGTGGTCTTCTCTCTCTCTCTCTCTCTCTCT 563  
Qy 361 GAGCCCGUGACCAAGCGCGAGAGUGCGGAGCGUGAUAAGAAACUACAAGCACUGCU 420  
Db 564 GAGCCAGTCAAAAGGCGAGAAATGCTGGAGAGTGTATCAAAATTAACAAGCACTGT 623  
Qy 421 CCGGAGAUUCUGGCAAGGCGCAGGAGCGCUGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480  
Db 624 CTTGAGATCTTCGCGCAAAAGCTCTGAGTCTCTGAGCTGGTCTTTGGCATTTGAG 683  
Qy 481 GAGCGCCAGCCACCGCGCACAGCUAGCUGUGUGAGCAGCUGCGUGGCGCUGAGCU 540  
Db 684 GAAGCAGACCCACCGGCCACTCTCTATGCTCTGTCTCTGTCTCTCTCTCTCTCTCT 743  
Qy 541 GGCUGUGGCGGCGCAACCAAGAUCAUCCCAAGACCGGCUUCUUGAUAUCUGUGUGUG 600  
Db 744 GGCCTGCTGGGTGATATATCATGATCATGCCCAAGACAGGCTTCTGTGATAATTGT 803  
Qy 601 AUGAUCGCCAUGAGGCGCGCCAGCGCCCGAGGAGGAGAGUAGUAGGAGGAGCAGCAG 660  
Db 804 ATGATTGCAATGGAGGCGCGCATGCTCTGAGGAGGAGAAATCTGGGAGGAGCTGAG 863  
Qy 661 AUGGAGUGUACGACGCGCGCAGCAGCAGCGCUACCGCGAGCGCCCGCAGCAGCAG 720  
Db 864 ATGGAGGTGTATGATGGAGGAGGACAGTGCCTATGGGAGGCCAGGAGCTGCTACC 923  
Qy 721 CAGGACCUUGUGCAGGAGAAUACCUUGAGUACCGCCAGGUGCCCGACAGCGACCCG 780  
Db 924 CAAGATTTGGTGACGAAAGTACTCTGGAGTACCGGCAGGTGCGGACAGTATCCGCA 983  
Qy 781 CGUACGAGUUCUGUGGCGCGCCCGCGCGCGCGCGCGAGCAGCAGCAGCAGCAGCAG 840  
Db 984 CGCTATGAGTTCCTGTGGGTGCCAAGGCGCTCGCTGAAACCAAGCTATGTGAAAGT 1043  
Qy 841 GAGUACGUGAUCAGGUGAGCGCGCGUGGCGUUCUUCUCCACCGCUGCGGAGGCC 900  
Db 1044 GAGTATGTGATCAAGGTCAAGTGTGCAAGAGTTGCGTTTTTCTTCCATCCCTG 1103  
Qy 901 GCCUGCGCGAGGAGGAGGCGGCGUGUGAGCCUGA 936  
Db 1104 GCTTTGAGAGGAGGAGGAGGAGTCTGAGCATGA 1139

RESULT 7  
US-09-468-433C-8  
; Sequence 8, Application US/09468433C  
; Patent No. 6680191  
; GENERAL INFORMATION:  
; APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR  
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS OF THE MAGE-C1  
; TITLE OF INVENTION: MAGE-B FAMILIES AND USES THEREOF









[illegible]



|    |      |  |      |
|----|------|--|------|
| Qy | 781  | CGCUACGAGUUCUGUGUGGGGGCCCCCGCGCCUGCGCGAGACCAAGUACAGUGAGAGUCCUG | 840  |
| Db | 1405 | CGCTATGAGTTCCTGTCGGGTCAGAGGGCCCTCGCTGAACACCACTATGTGAAGTCCCT    | 1464 |
| Qy | 841  | GAGUACGUGAUCAAGGUGAGCGCCCGCGUGCGCUUCUUUUUCCAGCCUGCGCGAGGCC     | 900  |
| Db | 1465 | GAGTATGTGATCAAGGTCAGTGCAAGAGTTGCGTTTTTCTTCCATCCTCGCGTGAAGCA    | 1524 |
| Qy | 901  | GCCUGCGCAGGAGGAGGGCGUGAGCCUGA                                  | 936  |
| Db | 1525 | GCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA                           | 1560 |

RESULT 14  
US-08-299-849B-7  
; Sequence 7, Application US/08299849B  
; Patent No. 5612201  
; GENERAL INFORMATION:  
; APPLICANT: De Plaen, Etienne; Boon-Palleur, Thierry;  
; APPLICANT: Leth, Bernard; Szkora, Jean-Pierre; De Smet, Charles;  
; APPLICANT: Chomez, Patrick  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In  
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022

|  |      |   |      |  |  |
|--|------|---|------|--|--|
| <b>Query Match</b>   |      |   |      |  |  |
| Best Local Similarity 67.1%; Score 629.6; DB 2; Length 2419;     |      |   |      |  |  |
| Matches 630; Conservative 121; Mismatches 184; Indels 1; Gaps 1; |      |   |      |  |  |
| Qy   | 1    | AUGAGCCUGGACGCGCAGCGCACUCGCAAGCCGAGGAGGCCUUGAGGGCCCACGACG   | 60   |  |  |
| Dd   | 626  | ATGTCTTGAGCAGAGGAGTGTGCACCTGCAGCCTTGAGAAGCCCTTGAGGCCCAACA   | 685  |  |  |
| Qy   | 61   | GAGGCCUUGGGCCUGUGUGUGUGAGCGCCGCCACCAGACGACGAGCCCCCUUGUGUG   | 120  |  |  |
| Dd   | 686  | GAGGCCUUGGGCCUUGUGUGUGUGAGCGCCGCCACCAGACGAGCCCCCUUGUGUG     | 745  |  |  |
| Qy   | 121  | GGCACCCUGGACGAGGUGCCACCGCGCGCAGCACGACCCCGCCAGAGCCCCCAGGGC   | 180  |  |  |
| Dd   | 746  | GGCACCCUGGACGAGGUGCCACCGCGCGCAGCACGACCCCGCCAGAGCCCCCAGGGC   | 805  |  |  |
| Qy   | 181  | GCCAGGCCUUCCCCACCAUCAUAUCCACCGCCGAGCCGACGAGCGAGGGCAGC       | 240  |  |  |
| Dd   | 806  | GCCTCGGCTTTCCCACTACCATCACTTCACCTCGACAGAGCAACCCAGTAGGGGTTC   | 865  |  |  |
| Qy   | 241  | AGCAGCGGAGAGGAGGGCCCCAGACACAGCUGCAUCCUGAGAGCCUUGUCCCGGCC    | 300  |  |  |
| Dd   | 866  | AGCAGCGGTGAAGAGGAGGGGCCAAGCACCTCTTGATCCTCGAGTCTTGTTCCGAGCA  | 925  |  |  |
| Qy   | 301  | GUCAGCACCAAGAAAGUGGCGCAGCUCUGUGGGGUUCGUCUGUGAAGUACCGCGCCG   | 360  |  |  |
| Dd   | 926  | GTAATCACTAAGAAAGTGGCTGATTGGTTGGTTCTGCTCTCAATATCAGCGCAGG     | 985  |  |  |
| Qy   | 361  | GAGCCCGUGAACCAAGGCCGAGAUUGUGGAGCGUGAUAAGAAUAACAAGCACUGCUC   | 420  |  |  |
| Dd   | 986  | GAGCCAGTCACAAGGCGAGAAATGCTGGAGAGTGTATCAAAAATTACAAAGCACTGTTT | 1045 |  |  |
| Qy   | 421  | CCGAGAUUUCGGCAAGGCCAGCAGAGCCUGCAGCUGGUGUGUUGGCAUCGAGGUAAG   | 480  |  |  |
| Dd   | 1046 | CCTTGAGATCTTCGGCAAGGCTCTGAGTCTCTGCAGCTGCTTTGGCATGAGTGAAAG   | 1105 |  |  |
| Qy   | 481  | GAGCGCAGCCCAACCGCCACAGCUAGCUGUGGUGACUGCCUGCGGCCUGAGCAAGC    | 540  |  |  |
| Dd   | 1106 | GAGCAGACCCCAACCGGCCACTCTATGTCTTGTCTCCTGCTAGGTCTCTCTATGAT    | 1165 |  |  |
| Qy   | 541  | GGCCUGCUGGGCGCAACACAGAUCAUCCCAAGACCGGCUUCUGAUCAUCGUGUGUG    | 600  |  |  |
| Dd   | 1166 | GGCCTGCTGGGTGATAATCAGATCATGCCCAAGCAGGCTTCTGTATATGTTCTCTGTC  | 1225 |  |  |
| Qy   | 601  | AUCAUCCCAUGAGGGCGGCCAGCGCCCGAGGAGGAGNAUCUGGAGGAGCUGAGCCUG   | 660  |  |  |
| Dd   | 1226 | ATGATTGCAATGAGAGGCGGCGCATGCTCTGAGAGGAAATCTGGGAGGAGCTGAGTGT  | 1285 |  |  |
| Qy   | 661  | AUGGAGGUGUACGACGGCGCGCAGCAGCGCCUAGCGGAGCCCGCGAAGCUGUGACCC   | 720  |  |  |
| Dd   | 1286 | ATGAGAGGTGATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGTCACC  | 1345 |  |  |
| Qy   | 721  | CAGGACUCUGUGCAGGAGAAGUACCUUGAGUACCGCCAGGUGGCCGACGACGACCCGCC | 780  |  |  |
| Dd   | 1346 | CAAGATTTGGTGAGGAAAGTACTCTGGAGTA-CGGCAGGTGCGCGACAGTGAATCCGCA | 1404 |  |  |
| Qy   | 781  | CGCUACGAGUUCUGUGGGGCCCCCGCGCCUGGCGGAGACAGCUACGUGAAGGUGCUG   | 840  |  |  |
| Dd   | 1405 | CGGTATGAGTTCCTGTGGGGTCCAGGGCCCTCGCTGAAACCAAGCTATGTGAANGTCTT | 1464 |  |  |
| Qy   | 841  | GAGUACGUAUCAAGGUGAGCGCCCGCGUGCGCUUCUUCUCCCAAGCCUGCGCAGGCC   | 900  |  |  |
| Dd   | 1465 | GAGTATGTGATCAAGGTGAGTGAAGAGTTCCGTTTTCTTCCCATCCCTCGCGTGAAGCA | 1524 |  |  |
| Qy   | 901  | GCCUCGCGGAGGAGGAGGGCGUGUGAGGCCUGA                           | 936  |  |  |
| Dd   | 1525 | GCTTTGAGAGAGGAGGAGGGAGTGCTGAGCATGA                          | 1560 |  |  |

RESULT 15  
US-08-142-368A-7  
; Sequence 7, Application US/08142368A  
; Patent No. 5925729













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QY 301 GUGAUCACCAAGAGGUGGCCGACCGUGGUGGCUUCCUGUGUGAAGUACCGCGCCGC 360
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Db 504 GTAATCACTAAGAAGTGGCTGATTTGGTTGGTTCTCTCTCTCAATATTCGAGCCAGG 563
QY 361 GAGCCGUGAGCAAGGCGAGAGUGUGGAGAGCGUGAUAAGAAUAUAAGACACUGCUUC 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 564 GAGCCAGTCAAAAGCGCAAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTGTTT 623
QY 421 CCCGAGAUUCGCGCAAGCCAGAGCCGAGAGCCUGGAGUGUUCGCGAUGAGCGAAG 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 624 CTGAGATCTTCGGCAAGCCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAATTGACGTGAAG 683
QY 481 GAGGCGGACCCCAACCGGCCACAGCUACGUGUGUGGACCGUGGCGGUGAGCUAGCAG 540
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 684 GAAGCAGACCCCAACCGGCCACTCTATGCTCTGTCACCTGCTAGGTCTCTCTATGAT 743
QY 541 GGCUGUGGCGGCAACACAGAUAGCCCAAGACCGGCUUCCUGAUAUGUGUGUGUG 600
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 744 GGCCTGCTGGGTGATAATCAGATCATGCCCCAAGACAGGCTTCTGATAATTGTCTGTC 803
QY 601 AUGAUCGCAUGGAGGCGGCCACGCCCGGAGGAGAGAUUGGAGGAGCGUGAGCGUG 660
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 804 ATGATTGCAATGGAGGCGGCCATGCTCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 863
QY 661 AUGGAGUGUACGACGCGCGGAGCACAGCGCCUACGCGAGCCCGCAAGCUGUGAC 720
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 864 ATGGAGGTGATATGGGAGGAGCAGATGCTATGGGAGCCAGGAGCTGCTACC 923
QY 721 CAGGACUGGUGCAGGAGAAAGUACUGGAGUACGCCAGGUGCCGACAGGACCCGCC 780
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Db 924 CAAGATTTGGTGCAAGAAAGTACCTGGAGTACCGGCAAGTGCAGATGATCCCGCA 983
QY 781 CGCUACGAGUUCUGUGGCGCCCGCGUGGUGGUGGUGGUGGUGGUGGUGGUGGUG 840
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 984 CGCTATGATTTCTGTGGGTCCAAAGGGCCCTCGCTGAAACGAGCTATGTGAAAGTCT 1043
QY 841 GAGUACGUGAUAAGGUGAGCGCCCGUGGUGGUGGUGGUGGUGGUGGUGGUGGUG 900
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Db 1044 GAGTATGATGACAGGTGAGTCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCA 1103
QY 901 GCCUGCGAGGAGGAGGAGGCGUGUGAGCCUGA 936
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Db 1104 GCTTTGAGAGAGGAGGAGGAGTCTGAGCATGA 1139
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## RESULT 6

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US-10-093-766-41
; Sequence 41, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpi, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 41
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 410721.1
US-10-093-766-41
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Query Match 68.3%; Score 641.6; DB 5; Length 2420;  
Best Local Similarity 67.4%; Pred. No. 8,1e-141;  
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

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Db 626 ATGTCTCTTGAGCAGAGAGGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACA 685
QY 61 GAGGCCUGGCGUGGUGUGGUGAGCGCGCCACACAGCAGCAGCAGCAGCAGCAGCAGCAG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 686 GAGGCCCTGGGCGCTGTGTGTGTCAGGCTGCCACCTCTCTCTCTCTCTCTCTCTCTG 745
QY 121 GGCACCCUGGAGGAGGUGGCCACCGCGGAGCAGCCAGCCCGCCAGAGAGCCCGCAGGGC 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 746 GGCACCTTGAGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 805
QY 181 GCCAGCGCUUCCGCCACCAUCAAUCUACCCGCGAGCCAGCCAGCAGGAGGAGCAGC 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 806 GCCTCCGCTTTCCCTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 865
QY 241 AGCAGCGCGAGGAGGAGGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 300
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Db 866 AGCAGCGCTGAAGAGGAGGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 925
QY 301 GUGAUCACCAAGAGGUGGCGACCTUGGUGGCGUUCUGUGUGAAGUACCGCGCCGC 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 926 GTAATCACTAAGAAGTGGCTGATTTGGTTGGTTCTCTCTCTCAATATTCGAGCCAGG 985
QY 361 GAGCCGUGACCAAGGCGGAGAGUGUGGAGAGCGUGAUAAGAAUAUAAGACACUGCUUC 420
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Db 986 GAGCCAGTCAAAAGGAGGAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGT 1045
QY 421 CCCGAGAUUCGCGCAAGGCGGAGAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1046 CTTGAGATCTTGGCAAAAGCCTCTGAGTCTCTGAGCTGGTCTTTGGCAATTGAGCTG 1105
QY 481 GAGCCGACCCCGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 540
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1106 GAAGCAGACCCCGCGCCACTCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1165
QY 541 GGCUGUGGCGCAACACAGAUCAUGCCCAAGACCGGCUUCCUGAUAUGGUGUGUG 600
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1166 GGCCTGCTGGGTGATATCAGATCATGCCCAAGACAGGCTTCTCTGATAATTGTCTG 1225
QY 601 AUGAUCGCAUGGAGGCGCGCCAGCGCCCGGAGGAGAGAUUCUGGAGGAGCAGCAGCUG 660
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1226 ATGATTGCAATGGAGGCGCGCCATGCTCTGAGGAGGAGAAATCTGGGAGGAGCTGAG 1285
QY 661 AUGGAGGUGUACGACGCGCGAGCAGCGCUACCGCGAGCCCGCGAGCAGCAGCAGCAG 720
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1286 ATGGAGGTGATATGGAGGAGGAGCAGTGCCTATGGGAGGCCAGGAAGCTGCTAC 1345
QY 721 CAGGACCCUGGAGGAGAAAGUACCGGAGUACCGCAGGUGCGCGAGCAGCAGCAGCAG 780
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1346 CAAGATTTGGTGCAGGAAAGTACCTGGAGTACCGCGAGGTGCGGAGACAGTATCCGCA 1405
QY 781 CGCUACGAGUUCUGUGGCGCCCGCGCGCCCGGAGCAGCAGCAGCAGCAGCAGCAGCAG 840
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1406 CGCTATGAGTTCTGTGGGTGCAAGGCGCCCTGCTGAAACAGCAGTATGTGAAAGTCT 1465
QY 841 GAGUACGUGAUAAGGUGAGCGCGCGUGGUGGUGGUGGUGGUGGUGGUGGUGGUG 900
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1466 GAGTATGTGATCAAGGTGAGTGAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCA 1525
QY 901 GCCUGCGGAGGAGGAGGCGGUGGAGCCUGA 936
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1526 GCTTTGAGAGGAGGAGGAGGAGTCTGAGCATGA 1561
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## RESULT 7

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US-10-802-250
; Sequence 250, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
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Db 1046 CTTGAGATCTTTGGCAAGCCTCTGAGTCTTTCAGCTGGTCTTTGGCAATTGACGTGAAG 1105
QY 481 GAGCGCGACCCACCGGCCACAGCUACGUGUGGACCUUGCGGCGGCGUGAGCUAGCAG 540
Db 1106 GAAGCAGACCCACCGGCCCTCTTATGCTCTTGTCTGCTTGTCTCTGCTTGTCTCTATGAT 1165
QY 541 GCGCUGUGGCGCAACACAGAUCAUGGCCAAGACCGGCUUCCUGAUCAUCUGUGUGUG 600
Db 1166 GSCCTGCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCTTGATAATTGTCTGTGTC 1225
QY 601 AUGAUGCGCAUGGAGGGGCGCCACCGCCCGAGGAGGAGAUUCUGGAGGAGCUGAGCUG 660
Db 1226 ATGATTGCAATGGAGGGGCGCATGCTCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285
QY 661 AUGAGGUGUACGACGGCGCGAGCACAGCGCUACGCGGAGCCCGCAAGCUGUGAGCC 720
Db 1286 ATGGAGGTGTATGATGGAGGAGGACACAGTGCCTATGGGAGCCACAGGAAGCTGCTACC 1345
QY 721 CAGGACCUUGUGCAGGAGAAGUACUGGAGUACCGCCAGGUGCCGACAGCGACCCCGCC 780
Db 1346 CAAGATTTGTTGTCAGGAAAGTACCTGGAGTACCGGCAGGTGCCGACAGTATCCCGCA 1405
QY 781 CGCUACGAGUUCUGUGGGGCGCCCGCGCCUGGCGGAGACAGCUAGCUAGAGUGUG 840
Db 1406 CGCTATGATTTCTGTGGGGTCCAAAGGGCCCTCGCTGAAACCAAGCTATGTGAAAGTCTT 1465
QY 841 GAGUACGUGAUCAGGCGCGCGUGGCGCUUUCUUCUCCAGCGGCGGAGGCC 900
Db 1466 GAGTATGTATCAAGGTCAAGAGTTCGCTTTTCTTCCATCCCTCGGTGAAGCA 1525
QY 901 GCCUCGCGGAGGAGGAGGCGGCGUGUGAGCCUGA 936
Db 1526 GCTTTGAGAGGAGGAGGAGGAGGAGTCTGAGCATGA 1561

RESULT 9
US-10-741-466-5
; Sequence 5, Application US/10741466
; Publication No. US20040180058A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003
; CURRENT APPLICATION NUMBER: US/10/741,466
; PRIOR FILING DATE: 2003-12-19
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-741-466-5

Query Match 68.3%; Score 641.6; DB 8; Length 2420;
Best Local Similarity 67.4%; Pred. No. 8.1e-141;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

QY 1 AUGAGCCUGGAGCAGCGCAGCGUGCAUGCAAGCCGAGGAGGCGCCUGAGGCGCCAGCAG 60
Db 626 ATGTCTCTTGGACGAGAGGTCTGCACCTGCAAGCTGAGGAAGCCCTTGAGGCCCNACAA 685
QY 61 GAGGCCUUGGCGUGUGUGUGAGCGCCGCGCCACAGCAGCAGAGCGCCCGUGUGUGUG 120
Db 686 GAGGCCUUGGCGUGUGUGUGAGCGCGCTGCGAGGCTGCCACCTCTCTCTCTCTCTGTC 745
QY 121 GGCACCUUGGAGGAGGUGCCACCGCGGAGCAGCCAGCCCGCCCGAGGCGCCCGAGGC 180
Db 746 GGCACCUUGGAGGAGGUGCCACCGCTGCTGGGTCAACAGATCTCTCCCGAGTCTCAGGGA 805
QY 181 GCCAGCGCCUUCGCCACCAACCAUCAAUUCACCGCGCAGCGCCAGCGCGGCGGAGG 240
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Db 806 GCCTCCGCTTTTCCACTACATCAACTTTCAGTCGACAGAGCAACCCAGTGAAGGTTC 865
QY 241 AGCAGCGCGAGGAGGAGGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 300
Db 866 AGCAGCGGTGAAGAGGAGGAGGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 925
QY 301 GUGAUAACCAAGAGGUGGCGGACCUUGGUGGCUUCCUGUGUGAAGUACCGCGCGCCG 360
Db 926 GTATCACTAAGAAGGTGGCTGATTGGTTGTTTCTGCTCTCAATATCAGAGCCAGG 985
QY 361 GAGCCUGUGACCAAGCGCGAGAUUCUGGAGGAGCGUGAUCAAGAAUAUAUAUAUAUAUA 420
Db 986 GAGCCAGTCAAAAGGCGAGAAATGCTGAGAGTGTATCAAAAATTCAAGCACTGTGTTT 1045
QY 421 CCCGAGAUUCUUGCGCAAGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480
Db 1046 CTTGAGATCTTGGCAAAAGCCTCTGAGTCTTTCAGCTGCTTTCGCAATTTGCGTGAAG 1105
QY 481 GAGGCCGACCCACCGGCCACAGCUACGUGUGUGAGCAGCAGCAGCAGCAGCAGCAGCAG 540
Db 1106 GAAGCAGACCCACCGGCCACTCTTATGCTCTTGTCACTGCTAGTCTCTCTCTATGAT 1165
QY 541 GGCUGUGGCGGCAACACCAUAUAUCCCAAGACCGGCUUCCUGAUCAUCUGUGUGUG 600
Db 1166 GGCCTGCTGGTGTATATCAGATCATGCCCAAGACAGGCTTCTGTATAATTGTCTGTGTC 1225
QY 601 AUGAUCGCCAUGAGGCGGCGCCAGCGCCCGAGGAGGAGAUUCUGGAGGAGCAGCAGCUG 660
Db 1226 ATGATTGCAATGGAGGGCGCCATGCTCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285
QY 661 AUGGAGGUGUACGACGCGCGCGAGCAGCAGCGCAGCGGCGGCGGCGGCGGCGGCGG 720
Db 1286 ATGGAGGTGTATGATGGAGGAGGAGCAGTGCCTATGGGAGGCCAGGAGGCTCTCACC 1345
QY 721 CAGGACCUUGUGCAGGAGAAGUACCUAGGAGUACCGCCAGGUGCCGACAGCGACCCCGCC 780
Db 1346 CAAGATTTGTTGTCAGGAAAGTACCTGGAGTACCGGCGAGTCCGCGACAGTATCCCGCA 1405
QY 781 CGCUACGAGUUCUUGUGGGCGCCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Db 1406 CGCTATGAGTTCTGTGGGGTCCAAAGGGCCCTCGCTGAAACCAAGCTATGTGAAAGTCTT 1465
QY 841 GAGUACGUGAUCAGGUGAGCGCGCGGUGGCGCUUUCUUCUCCAGCGCGGCGGAGGCC 900
Db 1466 GAGTATGTATCAAGGTCAAGTCAAGAGTTCGCTTTTCTTCCATCCCTCGGTGAAGCA 1525
QY 901 GCCUCGCGCAGGAGGAGGAGGCGGUGUGUGAGCCUGA 936
Db 1526 GCTTTGAGAGGAGGAGGAGGAGGAGTCTGAGCATGA 1561

RESULT 10
US-10-657-022-81
; Sequence 81, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
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Db 866 AGCAGCGTGAAGAGGGGGCCCAAGCACCTTTGTATCTTGGAGTCTTGTTCGGAGCA 925
Qy 301 GUGAUAACCAAGAGGUGGCGCGACCUUGUGGGUUCUUGUGUGAAGUACCGCGCCGC 360
Db 926 GTAATCACTAAGAAGTGGCTGATTGGTTGGTTTCTGCTCTCTCAATATCGAGCCAGG 985
Qy 361 GAGCCCGUGACCAAGGCGGAGAUUGUGGAGCGUGAUAAGAAACUAACAAGCACUGCUUC 420
Db 986 GAGCCAGTCAAAAGGAGAAATCTGGAGAGTGTCTATCAAAAATTACAAGCACTGTTTT 1045
Qy 421 CCCGAGAUUCUGCAAGGCCAGCGAGCCUGAGCGUGUGUGUGUUGGCAUCGAGUGAAG 480
Db 1046 CCTGAGATCTTCGCAAAAGCCTCTGAGTCTTGCAGCTGGTCTTGGCAATTGAGTGAAG 1105
Qy 481 GAGCCGACCCACCGGCCACAGCUAGUGUGUGAGACCUUGCGGCGGCGGCGUGAGCUAGC 540
Db 1106 GAAGCAGACCCACCGGCCACTCTATGTCTTGTCTACCTGCTAGGTCTCTCTATGAT 1165
Qy 541 GGCUGUGGGCGCAAAACCAUAUGCCCAAGACCGGCUUCCUGAUAUCUGUGUGUG 600
Db 1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCTCTGATAATTGTCTGCTC 1225
Qy 601 AUGAUCGCCAUGGAGGGCGCCACCGCCCGAGGAGGAGUUCUGGAGGAGCGUGAGUG 660
Db 1226 ATGATTCAATGGAGGGCGGCCATGCTCTCTGAGGAGGAATCTGGGAGGAGCTGAGTGTG 1285
Qy 661 AUGAGGUGUACAGCGCGCGAGCACAGCGCCUACCGCGAGCCCGCAAGCUCUGACCC 720
Db 1286 ATGGAGGTGTATGATGGAGGGAGCAGTGCCTATGGGAGCCCGAGGAGCTGCTCACC 1345
Qy 721 CAGGACCUUGUGAGGAGAAAGUACUUGAGUACCGCAGGUGCCCGACAGCACCGCCGC 780
Db 1346 CAAGATTTGGTCAGGAAAGTACTCTGGAGTACCGGAGGTGCGGACAGTGTATCCGCA 1405
Qy 781 CGCUACAGUUCUGUGGGCCCCCGCGCCUGGCGGAGCCAGCCAGCUAGGAGUGUG 840
Db 1406 CGCTATGAGTTCTGTGGGTCCAAAGGCCCCGCTGCTGAAACCACTATGTGAAAGTCTT 1465
Qy 841 GAGUACGUAUCAAAGGAGAGCGCGCGGUGGCUUUCUUCGCCAGCUGCGCGAGGCC 900
Db 1466 GAGTATGTATCAAGGTCAAGTGTGCAAGAGTTCGCTTTTCTTCCCATCTCCTGCGTGA 1525
Qy 901 GCCUGCGGAGGAGGAGGCGGUGUGAGCCUGA 936
Db 1526 GCTTTGAGAGAGGAGGAAGAGGAGTCTGAGCATGA 1561
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## RESULT 2

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US-11-178-134-6
; Sequence 6, Application US/11178134
; Publication No. US20060019290A1
; GENERAL INFORMATION:
; FILE REFERENCE: 030160
; APPLICANT: University of Pittsburgh - of The Commonwealth System of
; APPLICANT: Higher Education
; APPLICANT: Godfrey, Tony
; APPLICANT: Hughes, Steven
; APPLICANT: Xi, Liqiang
; APPLICANT: Gooding, William E
; APPLICANT: Raja, Siva E
; TITLE OF INVENTION: Identification of Markers in Esophageal Cancer, Colon Cancer,
; Head and Neck Cancer and Melanoma
; CURRENT APPLICATION NUMBER: US/11/178,134
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: 60/586,599
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/587,019
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1722
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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-178-134-6
Query Match 68.2%; Score 640; DB 12; Length 1722;
Best Local Similarity 67.3%; Pred. No. 1.8e-124;
Matches 630; Conservative 121; Mismatches 185; Indels 0; Gaps 0;
Qy 1 AUGAGCCUGAGCAGCGCAGCUGCAUCUGAACGCCGAGGAGGCCUUGGAGGCCCGCAGCAG 60
Db 188 ATGCTCTTTGAGCAGAGGAGTCTGCATCTGCAAGCCTGAGGAAGCCCTTGGAGGCCCAAA 247
Qy 61 GAGGCCUGGGCUGUGUGUGCGGCGCCACACGAGCAGCAGCAGCAGCAGCAGCAGCAGC 120
Db 248 GAGGCCCTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 307
Qy 121 GGCACCCUGAGGAGGUGGCCACCGCGCGCAGCACCGACCCCGCCAGAGAGCCCGCCAGGGC 180
Db 308 GGCACCTGGAGGAGGTGCCCACTGTCTGGGTCAACAGATCTCTCCAGAGTCTCTCAGGGA 367
Qy 181 GCAGCGCCUUCCCCACCAUCAAUCCUACCCGCCAGCGCCAGCCAGCCAGCGAGGCGAGC 240
Db 368 GCCTCGGCTTTCCCACTACCATCACTTCACTCGACAGAGGCAACCAGTGTGAGGTTC 427
Qy 241 AGCAGCGCGAGGAGGAGGCGCCCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 300
Db 428 AGCAGCGGTGAAGAGGAGGGGCCAAGCACCTTGTGTATCTTGGAGTCTTGTTCGAGCA 487
Qy 301 GUGAUAACCAAGAGGUGGCGGACCUUGUGGGGCUUCCUGUGUGAAGUACCGCGCCGC 360
Db 488 GTAATCACTAAGAAGTGGCTGATTGGTTGGTTTCTGCTCTCAAAATATCGAGCCAGG 547
Qy 361 GAGCCCGUGACCAAGGCGGAGUUGUGGAGCGUGAUAAGAAACUAACAAGCACUGCUUC 420
Db 548 GAGCCAGTCAAAAGGCGAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTGTTT 607
Qy 421 CCCGAGAUUCUGGCGAGGCCAGCGAGCUCGAGCUGGUGUUCGSCAUCGAGCUGAAG 480
Db 608 CCTGAGATCTTCGGCAAAAGCCTCTGAGTCTTGCAGCTGGTCTTGGCATGTGAGTGAAG 667
Qy 481 GAGGCCACCCACCGGCCACAGCUGCUGUGUGAACCUUGCCUGGGGCCUGAGCUAGCAGC 540
Db 668 GAAGCAGACCCACCGGCCACTCTATGTCTTGTCTACCTGCTAGGTCTCTCTATGAT 727
Qy 541 GGCUGUGGGCGACAAACAGAUCAUGCCCAAGACCGGCUUCCUGAUAUCGUGUGUGUG 600
Db 728 GGCCTGTGCTGGTGTATTAATCAGATCATGTCCCAAGACAGGCTTCTGTGATAATTGTCTG 787
Qy 601 AUGAUCGCCAUGGAGGCGGCCACCGCCCGAGGAGGAGAUUCUGGAGGAGCUGAGCUG 660
Db 788 ATGATTGCAATGGAGGGCGGCCATGTCTCTGAGGAGGAATCTGGGAGGAGCTGAGTGTG 847
Qy 661 AUGAGGUGUACGACCGGCCCGCGAGCACAGCGCCUACCGCGAGCCCGCCCAAGCUGAGC 720
Db 848 ATGGAGGTGTATGATGGGAGGAGCAGTGCCTATGGGAGGCCCGCAGAGGCTCTCACC 907
Qy 721 CAGGACCUUGUGCAGGAGAAAGUACCUUGAGUACCGCCAGGUGGCCGAGCAGGAGCCGCC 780
Db 908 CAAGATTTGGTGCAGGAAAGTACTCTGAGTACCGGAGGTGCGGAGCAGTGTATCCGCA 967
Qy 781 CGCUACAGUUCUGUGGGGCCCGCGCCCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 840
Db 968 CGCTATGAGTTCTGTGGGTTCCAAGGGCCCTTGTCTGAAACCACTATGTGAAAGTCTT 1027
Qy 841 GAGUACGUGAUAAGGUGAGCGCCCGCGUGCGCUUUCUUCUCCCGCAGCUGCGAGGCC 900
Db 1028 GAGTATGTGATCAAGGTCAAGTGTGCAAGAGTTCGCTTTTCTTCCATCTCCGCGTGA 1087
Qy 901 GCCUGCGCAGGAGGAGGAGGCGUGUGAGCCUGA 936
Db 1088 GCTTTGAGAGGAGGAAGAGGAGTCTGAGCATGA 1123
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; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 946082
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-946082

Query Match      21.3%; Score 200; DB 6; Length 604;
Best Local Similarity 58.0%; Pred. No. 6.6e-33;
Matches 268; Conservative 42; Mismatches 131; Indels 21; Gaps 1;

Qy 1 AUGAGCCUGGAGCAGCGCCUGCAUGCAAGCCCGAGGAGGCCUGGAGGCCAGCAG 60
Db 143 ATGCTCTTTCAGAGAGAGTCTGAGGCTGAGGAGGCTTGCACACCAAGAA 202
Qy 61 GAGGCCUGGCGUGGUGGUGGUGGAGGCGGCCCGCCACCG-----C 99
Db 203 GAGGCCCTGGGCCCTGGTGGGTGTGCAGGCTGCCACTAGTAGGAGCAGGAGGCTGTGTC 262
Qy 100 AGCAGCAGCCCGCCUGGUGGUGGCGCACCCUGGAGGAGGUGCCACCGCGCGGAGCAGCCGAC 159
Db 263 TCCTCTCTCTCTGCTGCTCCAGGACACCTCTGGGGAGGTGCTGTGCTGGTTCACCGGT 322
Qy 160 CCCCCCAGAGCCCGCCAGGCGCCAGGCGCCUUCUCCACCAUACUACUACUACUACUACUACUAC 219
Db 323 CCTCTCAAGAGTCTCTCAGGAGGCGCTCCGCCATCCCACTGCCATCTGCTATG 382
Qy 220 CGCAGCCAGCGAGGCGAGCAGCGCCGCGAGGAGGAGGCGCCAGCAGCAGCAGCAGCAGCAGC 279
Db 383 AGGCAATTCATTAAAGGGCTCAGCAACCAAGAGAGGAGGAGGCGCAAGCCTCCCTGAC 442
Qy 280 CUGGAGAGCCUGUUCGCGCGUGAUACCAAGAGGUGGCGCACCCUGGUGGCGUUCUG 339
Db 443 CCAGAGTCTGTGTTCCGAGCAGCACTCAGTAAAGAGTGGCTGACTTGATTCATTTCG 502
Qy 340 CUGUGAAGUACCGCGCCCGAGCGCCUGAGCCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 399
Db 503 CTCCTCAAGTATTAAAGTCAAGGAGCGCGTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 562
Qy 400 AAGAACUACAGCAGCUGUUCGCCGAGAUUCUCCGAGAGGCC 441
Db 563 AAAAATACAGCGCTGCTTCTCTGTGATCTTCGGCAAGGCC 604
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RESULT 9
US-09-925-065A-349229
; Sequence 349229, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
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; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 349229
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-349229

Query Match      21.2%; Score 198.6; DB 6; Length 560;
Best Local Similarity 50.6%; Pred. No. 1.3e-32;
Matches 273; Conservative 62; Mismatches 195; Indels 9; Gaps 1;

Qy 158 ACCCCCCCAGAGCCCCCAGGCGCCAGCGCCUUCUCCACCAUACUACUACUACUACUACUACUAC 217
Db 16 ATCCTCCCCAGAGTGTCTCAGATAGCTCTCTCCCTCGTGGTTCCTTCCAT 75
Qy 218 AGCGCCAGCCCGAGGCGCAGCAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 277
Db 76 TAGATCAATCTGATAGGGCTCCAGCAGCCAAAGAGGAGGAGTCCCAAGCACCTACAGG 135
Qy 278 UCCUG-----GAGAGCCUGUUCGCGCCCGUGAUACCAAGAGGUGGCGGACCUAG 328
Db 136 TCCTGCCAGACAGTGTCTTTACCCAGAAAGTGAGATAGATGAAAGAGTGACTGATTGG 195
Qy 329 UGGGUUCCUGUGUGUAGUACCGCGCCCGGAGCCCGUGACCAAGGCCGAGUAGUAGUAGUAGUAG 388
Db 196 TGCAGTTTCTGCTTCTCAAGTATCAATGAAGAGGCGGATCAAAAGGCGAGAAATATCTGG 255
Qy 389 AGAGCGUGAUACAAGACUACAGCAGCUGCUUCCCGAGAUUCUCCGCAAGGCCAGCGAGA 448
Db 256 AGAGTGTCAATAAATATTAAGACCACTTCCCTTTGTTTAGTGAAGCCTCCGAGT 315
Qy 449 GCCUGCAGCUGGUGUGCAUCAGCAGUGAAGAGGCGGACCCACCGCGCACAGUACG 508
Db 316 GCATGCTGCTGCTTTGGCATTGATGTAAGGAAGTGGATCCCACTGGGCACTCTTTG 375
Qy 509 UGCUUGAGCUGCCUGGCGCUGAGCUACGACGCGCUGGUGGCGCAACCAAGAUCAUAGC 568
Db 376 TCCTTGTCACTCCCTCGGCTCCCTATGATGGATGCTGAGTGTCCAGAGCATGC 435
Qy 569 CCAAGACCGGCUUCUGAUCAUCUGUGUGUGUGAUUGCGCAUGGAGGCGGCCACGCC 628
Db 436 CCAAGCTGGCATTCATCTACTTATCTTAAGCATAGTCTTCATAGAGGGCTACTGCACCC 495
Qy 629 CCGAGGAGGAGUUCUGGAGGAGGAGCUGAGCGUGAGGUGUAGUACGAGCGGCGGAGCAG 687
Db 496 CTGAGGAGGTCTATCTGGGAAGCACTGAATATATGATGGGCTGTATGATGGATGGAGCAG 554

RESULT 10
US-09-925-065A-349230
; Sequence 349230, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
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; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 349230  
; LENGTH: 560  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-349230

Query Match 21.2%; Score 198.6; DB 6; Length 560;  
Best Local Similarity 50.6%; Pred. No. 1.3e-32;  
Matches 273; Conservative 62; Mismatches 195; Indels 9; Gaps 1;  
  
QY 158 ACCCCCCCAGAGCCCGAGGGCGCAGCGCCGCGAGGAGGGCCCGCAGCAUACUACCGCC 217  
Db 16 ATCTCTCCCGAGAGTCTCAGATAGCTCTCTCCCTCCCTCGGTCTGCTCCCTTCCAT 75  
  
QY 218 AGCGCAGCCCGAGGCGCAGCAGCGCGCGAGGAGGGCCCGCAGCAGCCAGCAGUCA 277  
Db 76 TAGATCAATCTGATGAGGGCTCCAGCAGCCAAAAGAGAGAGTCCAAAGCACCTTACAGG 135  
  
QY 278 UCCUG-----GAGAGCCUGUUCGCGCGCGUGAUCACCAAGAGUGGCGCGACUUG 328  
Db 136 TCCTGCCAGACAGTGTGAGTCTTTACCCAGAAAGTGAGATGATAAAGGCTGACTGATTGG 195  
  
QY 329 UGGGCUUCUGUGUGAGUACCGCGCGCGCGCGCGCGGAGCCGUGACCAAGGCGGAGUUGCG 388  
Db 196 TGCAGTTTCTGCTCTTCAAGTATCAAAATGAAGAGCGCGATCAAAAGGCAGAAAATACTGG 255  
  
QY 389 AGAGCGUGAUAAGAAACUACAAGACUCUGUCCCGCGAGUUCUUGCGCAAGCGCAGCGAGA 448  
Db 256 AGAGTGTCAAGAATATGAGACCACTTCCCTTTGTTGTTAGTGAAGCTCCGAGT 315  
  
QY 449 GCUUGAGUGUGUUGCGGACUGAGUAGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 508  
Db 316 GCATGCTGTGCTTTGGCATTTGATGTAAGAGAAAGTGGATCCCACTGCCACTCCTTTG 375  
  
QY 509 UGUGUGAGUGUGUGGCGCGUGAGUAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 568  
Db 376 TCCTTGTCACTTCCCTGGGCGTCACTATGATGGGATGCTGAGTGTATCCAGAGCATGC 435  
  
QY 569 CCAAGACCGGCUUCUGAUAUCUGUGUGUGAUGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 628  
Db 436 CCAAGACTGGCATTTCTCATCTTATCTTAAGCATATTTTATAGAGGGCTACTGCACC 495  
  
QY 629 CCGAGGAGAGUACUGGAGGAGCGUGAGUGAGUGAGUGAGUGAGUGAGUGAGUGAGUGAG 687  
Db 496 CTGAGGAGTCACTGGGAAGCACTGAATATGATGGGCTGTATGGGATGGAGCAC 554

RESULT 11  
US-11-044-051-72  
; Sequence 72, Application US/11044051  
; Publication No. US2005025553A1  
; GENERAL INFORMATION:  
; APPLICANT: VAN PEL, Aline  
; APPLICANT: GODELAINE, DanisLe  
; APPLICANT: CARRASCO, Javier  
; APPLICANT: BRASSEUR, Francis  
; APPLICANT: BOON-FALLEUR, Thierry  
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF  
; FILE REFERENCE: LUD 5888 US  
; CURRENT APPLICATION NUMBER: US/11/044,051  
; PRIOR FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: US 60/459,263  
; PRIOR FILING DATE: 2004-02-09  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 72  
; LENGTH: 1983  
; TYPE: DNA

;  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1329)..(1329)  
; OTHER INFORMATION: n at position 1329 is "a" in MAGE-C2 and "g" in CT10  
US-11-044-051-72

Query Match 21.1%; Score 198.4; DB 12; Length 1983;  
Best Local Similarity 49.3%; Pred. No. 1.3e-32;  
Matches 307; Conservative 72; Mismatches 232; Indels 12; Gaps 3;  
  
QY 311 AGAAGUGGCGCAGCUGGUGGCGUUCUGUGUGAAGUACCGCGCGCGAGCCGUGA 370  
Db 757 AAAAGGTGGCGAGTTAGTGAGTCTCTCTCAAAATACGAAGCAGAGGAGCGCTGAA 816  
  
QY 371 CCAAGGCGGAGUACUACAGACGAGUACGAGACUACAGCACUUGUCCCGGAGAU 430  
Db 817 CAGAGGCGAGAGATGCTGATGTTGTCATCAAG---TACAAAGATTACTTCTGTGATAC 873  
  
QY 431 UCGGCAAGGCGCAGCAGAGCGCUGCAGCUGUGUGUGCGCAUCGAGGAGGAGGCGGACC 490  
Db 874 TCAAGAGGCGCGTGAGTTCATGAGCTTCTTTTGGCCTTGCCCTGATAGAGTGGGCC 933  
  
QY 491 CCACCGGCGCAGCAGCUGUGUGAGCUGGCGCGUGGCGCGUGAGUACGAGCGCGUGCG 550  
Db 934 ---CTGACCACCTTCTGTGTGTTTGCAAAACACAGTAGGCTCAGCGATGAGGG---TA 984  
  
QY 551 GCGACACCCAGAUACGCGCCCAAGACCGCUUCUGAUCUUGUGUGAGUACGCGCA 610  
Db 985 GTGATGATGAGGGGCATGCGCGAGAAACAGCCTCTCTGATTTATTCTGAGTGTGATCTTCA 1044  
  
QY 611 UGAGGCGCGCGCAGCGCGCGGAGGAGAGUUGGAGGAGCGUGAGUGAGGAGUGU 670  
Db 1045 TAAAGGCGCACTGTGCTCTTGAGGAGGTCTCTGGAAGTCTGAATGTCAGTAGGGGTAT 1104  
  
QY 671 ACGAGCGCGCGAGCACAGCGCCUACCGCGAGCGCCCGAAGCGCGCGCGCGCGCGCGCG 730  
Db 1105 ATGCTGGGAGGAGCACTTCTGTCTTCTGAGGAGCGCTAGGAGGCTCTCACTAAAGTTTGG 1164  
  
QY 731 UGAGGAGAGUACUACCGGAGUACCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 790  
Db 1165 TGCAGGAGCACTTACCTGGAGTATCGGAGGTCGCGCGCGCGCGCGCGCGCGCGCGCG 1224  
  
QY 791 UCCUGGGGCG 850  
Db 1225 TCTGTGGGCTTCAAGAGCCCATTCAGAAAGCATCAAGAAAGTACTAGAGTTTTAG 1284  
  
QY 851 UCAAGGUGAGCGCGCGCGUGCGCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUC 910  
Db 1285 CCAAGCTGAACAACACTGTTCTAGTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1344  
  
QY 911 AGGAGGAGGCGGCGUGAGGCC 933  
Db 1345 ATGTGAAGAGAGAGTCCAGGCC 1367

RESULT 12  
US-11-044-051-104  
; Sequence 104, Application US/11044051  
; Publication No. US2005025553A1  
; GENERAL INFORMATION:  
; APPLICANT: VAN PEL, Aline  
; APPLICANT: GODELAINE, DanisLe  
; APPLICANT: CARRASCO, Javier  
; APPLICANT: BRASSEUR, Francis  
; APPLICANT: BOON-FALLEUR, Thierry  
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF  
; FILE REFERENCE: LUD 5888 US  
; CURRENT APPLICATION NUMBER: US/11/044,051  
; PRIOR FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: US 60/459,263  
; PRIOR FILING DATE: 2004-02-09  
; NUMBER OF SEQ ID NOS: 111















Db 735 GCAGGCTTACCAGAAACGATGGGAGTGCATAATGCAGCGATTCAAGTGATC 785

RESULT 3  
US-09-762-861B-1  
; Sequence 1, Application US/09762861B  
; Patent No. 6579528  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)  
; CURRENT APPLICATION NUMBER: US/09762,861B  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (673)..(673)  
; OTHER INFORMATION: At nucleotide 673, x = a or g  
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val  
; US-09-762-861B-1

Query Match 62.9%; Score 487.4; DB 3; Length 1023;  
Best Local Similarity 76.9%; Pred. No. 1.8e-83;  
Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;

Qy 1 AGATCTAAAGATGACCTGTGACCGAGGTGGAGACCTACTGCTGAGCATCATCCCCAG 60  
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGCAACGCTACGTTCTCTATCGTACCATC 74  
Qy 61 CGGCCCCCTGAAGCCGAGATCGCCAGAGCTGGAGACGTGTTCGCCGCGCAAGACAC 120  
Db 75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTGTCACTCTGACTAA 134  
Qy 121 CGACTGAGGTGCTGTGATGGAGTGGCTGAAGACACGAGCCCATCTGAGCCCCCTGACCAA 180  
Db 135 CGATCTTGAGGCACTCATGGAATGGCTTAAGACAGACCAATCTGTCACTCTGACTAA 194  
Qy 181 GGGCATCTGGGCTTCGTGTTCACTTACCGTGCAGCGCCAGCGCGCTTCGACGCGC 240  
Db 195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTCCCGAGTGGAGGACTGCAGCGTAG 254  
Qy 241 CGCTTCTGAGAACGCCCTGAAGCGCAACGGCGACCCCAACCAACATGGAAGAGCGGT 300  
Db 255 ACGCTTTGTCCAAATGCGCTTAGTGGAAACGGAGATCCAAACCAACATGGAAGAGCAGT 314  
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACTTCCAGCGCGCCCAAGGAGATCAGCCT 360  
Db 315 AAAAGTGTACAGGAAGCTTAAAGAGAAATTAACATTCATGGGGCAAAAGGTGGCACT 374  
Qy 361 GAGCTACAGCGCGCGCTTCGGCCAGCTGATGGGCTGATCTACAAACAGGATGGGCGC 420  
Db 375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCTGGAATCATATACAAACAGAAATGGAAC 434  
Qy 421 CGTGACCAACGAGGTGGCTTCGGGCTTGGGCTGCTGCGCCACCTTCGAGAGCAAGATCGCGCAG 480  
Db 435 TGTGACAAACCAAGTGGCAATTTGGCTTGTGCTGATGGCCCACTGTGAACAGATCGTGTATTC 494

Qy 481 CCAGCACCGCAGCCACAGGAGATGGTGACCAACCAACCAACCCCTGTATCAGGCGACGAA 540  
Db 495 CCAGCATCGATCTCACAGGCGAGATGGTGACCAACCAACCAACCCCTGTATCAGATGAA 554  
Qy 541 CAGGATCGTCTGGCCAGCACCAACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCGGA 600  
Db 555 CAGAAATGGTATTAGCCAGTACCGCGCTAAAGCCATGGAGCAGATGGCAGGGTCAGTGA 614  
Qy 601 GCAGGCCCGCAGGCGCATGGAGGTGGCCAGCAGGCGAGGCGAGATGGTGAGGCGCATGAG 660  
Db 615 GCAGGCGAGAGGCCCATGGAGGTGGCTAGTAGGCTAGGCGAGATGGTRCAGGCCAATGAG 674  
Qy 661 GACCATCGGCACCCACCCAGCAGCAGCGCGGCTGAAAGAACCACTGTGTGGAACCT 720  
Db 675 AACCATTTGGGACCCACCCCTAGCTCCAGTCCGCGTTTGAAGATGATCTCTCTTGA 734  
Qy 721 GCAGGCGCTACCAAGAGCGCATGGCGGTGCAGATGCAGCGCTTCAAGTGAAC 771  
Db 735 GCAGGCGCTACCAAGAGCGCATGGCGGTGCAGATGCAGCGATTCAAGTGATC 785

RESULT 4  
US-10-065-133A-1  
; Sequence 1, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (673)..(673)  
; OTHER INFORMATION: At nucleotide 673, x = a or g  
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val  
; US-10-065-133A-1

Query Match 62.9%; Score 487.4; DB 3; Length 1023;  
Best Local Similarity 76.9%; Pred. No. 1.8e-83;  
Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;

Qy 1 AGATCTAAAGATGAGCCTGTGACCGAGGTGGAGACCTACTGCTGAGCATCATCCCCAG 60  
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGCAACGCTACGTTCTCTATCGTACCATC 74  
Qy 61 CGGCCCCCTGAAGCCGAGATCGCCAGAGCTGGAGACGTGTTCGCCGCGCAAGACAC 120  
Db 75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTGTCACTCTGACTAA 134  
Qy 121 CGACTGAGGTGCTGTGATGGAGTGGCTGAAGACACGAGCCCATCTGAGCCCCCTGACCAA 180  
Db 135 CGATCTTGAGGCACTCATGGAATGGCTTAAGACAGACCAATCTGTCACTCTGACTAA 194  
Qy 181 GGGCATCTGGGCTTCGTGTTCACTTACCGTGCAGCGCCAGCGCGCTTCGACGCGC 240  
Db 195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTCCCGAGTGGAGGACTGCAGCGTAG 254

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Qy 241 CCGCTTCGTGCGAGAACCCCTGAAACGCAAGCGGACCCCAACACATGACAAAGGCCGT 300
Db 255 ACGCTTTGTCCAAAATGCCCTTAGTGGAACCGGAGATCCAAACAAACATGGACAGAGCAGT 314
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACCTTCACCGGCGCCAAAGGAGATCAGCCT 360
Db 315 AAAAAGTGTACAGGAAGCTTAAAGAGAAATAACATTCATCCATGGGCAAAAAGGTGGCACT 374
Qy 361 GAGCTACAGCGCGCGCGCCCTGGCCAGCTGCATGGGCTGATCTACAAACAGGATGGCGCG 420
Db 375 CAGCTATTCCACTGGTGCACCTAGCCAGCTGCATGGGACTCATATACAAACAGAAATGGGAAC 434
Qy 421 CGTGACACCGAGGTGGCCCTTGGCCCTTGGCTGGTGGCCACCTGCAGAGCAGATGCCCGACAG 480
Db 435 TGTGACAAACGGAAGTGGCCATTTGGCCCTGGTATGGCCACATGTGAAACAGATCGCTGATTC 494
Qy 481 CCAGCAGCGGAGCCACAGGAGATGTGACACCAACCAACCCCTGATCAGGACACGAGAA 540
Db 495 CCAGCATGTATCTCAGAGCGAGATGGTGAACAAACCAACCCATTAATCAGACATGAAAA 554
Qy 541 CAGGATGGTGTGGCCAGCACCAACCGCCAGGCGCATGGAGCAGATGGCCGCGCAGCAGCGA 600
Db 555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614
Qy 601 GCAGGCCCGGAGGCCATGAGGTGGCCAGCCAGCCAGCCAGGAGATGGTCAGGCCATGAG 660
Db 615 GCAGGCAGCAGAGGCCATGAGAGGTGCTAGTAGGCTAGGACAGATGTCAGGCAATGAG 674
Qy 661 GACCATCGGACCCACCCAGCAGCAGCGCGGCTGAAGAACGACCTGCTGGAGAACCT 720
Db 675 AACCATTTGGAGACCCACCTAGCTCAGTGCCGGTTTGAAGATGATCTCCTTGAATAATT 734
Qy 721 GCAGGCTTACCAGAAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
Db 735 GCAGGCTTACCAGAAACGGATGGGAGTGCRAATGCAGGATTCAGGTGATC 785

RESULT 5
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1
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Query Match 62.9%; Score 487.4; DB 3; Length 1023;  
Best Local Similarity 76.9%; Pred. No. 1.8e-83;

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Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;
Qy 1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACTAGTCTGAGCATCATCCCCAG 60
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGGAACGTACGTTCTCTCTATCGTACATC 74
Qy 61 CGGCCCCCTGAAGGCGAGATCGCCAGAGGCTGGAGGACGTGTTCCGCGGCAAGAACAC 120
Db 75 AGGCCCCCTCAAAAGCCGAGATCGCGCAGAGACTTGAAGATGTTTTCAGGGGAAGAACAC 134
Qy 121 CGACCTTGGAGGTGCTGATGGAGTGGCTGAAGACAGGCCCCATCTCGAGCCCCCTGACCAA 180
Db 135 CGATCTTGGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCTCTGACCTCTGACTAA 194
Qy 181 GGGCATCTCTGGGCTTCTGTTTCACTGACCTGACCTGCGGAGGCGGCGCTGAGGCGCG 240
Db 195 AGGGATTTTAGGATTCGTATTTCACGCTCACCGTCCCGTGGCGAGTGGAGGAGCTGAGCGGTAG 254
Qy 241 CCGCTTCGTGCAGAACCGCCTGAACCGCAACGGCGACCCCAACAAACATGGAACAGGCCGT 300
Db 255 ACGCTTTGTCCAAAATGCCCTTAGTGAACCGAGATCCAAACAAACATGGAACAGGAGT 314
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACTTTCAGCGGCGCAAGGAGATCAGCCT 360
Db 315 AAACTGTACAGGAAGCTTAAAGAGAGAAATAACATTCATGGGCAAAAAGGCTGGCACT 374
Qy 361 GAGCTACAGCGCGCGGCGCCTTGGCCAGCTGCATGGGCGCTGATCTACAAAGGATGGCGC 420
Db 375 CAGCTATTTCACCTGGTGCACCTAGCCAGCTGCATGGGACTCATATACAAAGAAATGGGAAC 434
Qy 421 CGTGACCAACCGAAGTGGCATTTGGCCCTGGTATGCGCCACATGTGAACAGATCCCTGATTC 494
Qy 481 CCAGCAGCGCAGCCACAGCAGATGTGTACCAACCAACCCCTGATCAGGCAACGAGAA 540
Db 495 CCAGCATGATCTCAGAGCAGATGTGTGAACAAACCAACCCATTAATCAGACATGAAAA 554
Qy 541 CAGGATGGTGTGGCCAGCACCAACCGCCAGGCGCATGGAGCAGATGGCCGCGCAGCAGCA 600
Db 555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGA 614
Qy 601 GCAGGCCCGGAGGCCATGAGGTGGCCAGCCAGGCGCAGGCGCAGATGGTCAGGCGCATGAG 660
Db 615 GCAGGCAGCAGAGGCCATGAGAGGTGCTAGTAGGCTAGGACAGATGTCAGGCAATGAG 674
Qy 661 GACCATCGGACCCACCCAGCAGCAGCGCGCTGAAGAACGACCTGCTGGAGAACCT 720
Db 675 AACCATTTGGGACCCACCTAGCTCAGTGCCGGTTTGAAGATGATCTCCTTGAATAATT 734
Qy 721 GCAGGCTTACCAGAAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
Db 735 GCAGGCTTACCAGAAACGGATGGGAGTGCRAATGCAGGATTCAGGTGATC 785

RESULT 6
US-08-809-513A-6
; Sequence 6, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
```



MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage  
COMPUTER: Gateway Pentium II  
OPERATING SYSTEM: Windows 98  
SOFTWARE: Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/909,513A  
FILING DATE: 24-MAR-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03663  
FILING DATE: 18-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94115505.3  
FILING DATE: 30-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Kurt G. Briscoe  
REGISTRATION NUMBER: 33,141  
REFERENCE/DOCKET NUMBER: Hobom 9832-KGB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 332-1700  
TELEFAX: (914) 332-1844  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6802 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Influenza virus, RNA sequence  
INDIVIDUAL ISOLATE: pHL1191  
US-08-809-513A-6

Query Match 62.8%; Score 486.6; DB 3; Length 6802;  
Best Local Similarity 77.3%; Pred. No. 3.1e-83;  
Matches 591; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

Qy 7 AAAGATGACCTGCTGACCGAGGTGGAGACCTAGTGTGATGATCATCCCCAGGGGCC 66  
Db 34 AAAGATGAGTCTTAAACCGAGGTGCGAAACGTACGTTCTCTATCATCCCGTCAGGGCC 93  
Qy 67 CCTGAAGCCGAGATCGCCAGAGGCTGGAGAGCTGTTCGCCGCGCAAGAACACCGACCT 126  
Db 94 CCTAAAGCCGAGATCGCACAGACTTGAAGATGTCTTTCAGGGAAGAACCGATCT 153  
Qy 127 GGAGGTGCTGATGGAGTGGCTGAAGACAGGCCCCATCTGAGCCCCCTGACCAAGGGCAT 186  
Db 154 TGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACTCTGACTAAGGGAT 213  
Qy 187 CTGGGCTTGTGTTTCAACCCTGACCGTCCAGAGGCGCGGCTGACGCGCGCGTT 246  
Db 214 TTTAGGATTTGTGTTTCAAGCTCAGCGTCCAGTGGAGGAGACTGCGAGCGTAGACGCTT 273  
Qy 247 CGTCAGAACGCTTGAAGCGCAACGGGACCCCAACAACATGACCAAGGCGCGTGAAGCT 306  
Db 274 TGTCCAAATGCCCTTAAATGGGAACGGGGATCCAAATAAATGACCAAGCAGTTAAACT 333  
Qy 307 GTACAGGAAGCTGAAGAGGAGATCACCTTCCAGGCGCCCAAGGAGATCAGCCTGAGCTA 366  
Db 334 GTATAGGAAGCTCAAGAGGAGATAACATTCATGGGGCCAAAGAAATCTCACTCAGTTA 393  
Qy 367 CAGCGCGGCGCTTGGCCAGCTGATGGGGCTGATCTAACAAGGATGGCGCGCGTGC 426  
Db 394 TTCTGCTGGTCACTTGGCACTTGTATGGGGCTCATATACCAAGGATGGGGGCTGTGAC 453  
Qy 427 CACCGAGTGGCTTCCGCTGCTGTGCGCCACCTGCGAGCAGATCGCCGACACGCA 486  
Db 454 CACTGAAGTGGCATTTGGCCCTGGTATGTGCAACCTGTGAAACAGATTCCTGACTCCCAGCA 513  
Qy 487 CCGAGGCCACAGGAGATGGTGACCACCAACCCCTGATCAGGCGACAGGAACAGGAT 546

Db 514 TCGGTCTCATAGGCNAATGGTGACAAACAACCAACCCCACTAATCAGACATGAGAAACAGAA 573  
Qy 547 GGTGCTGCGCAGACCAACCCGAGGCGCATGGAGCAGATGCCGCGCAGCAGCAGCAGGC 606  
Db 574 GGTTTTAGCCAGCACTACAGTAAGGCTATGGAGCAAAATGGCTGGATCGAGTGAAGCAAGC 633  
Qy 607 CGCGAGGCCATGGAGGTGGCCAGCCAGGCGCAGGCGCAGATGGTGAGGCCCATGAGGACCAT 666  
Db 634 AGCAGAGGCCATGGAGGTGCTAGTCAGGCTAGGCAAAATGGTGCAAGCGATGAGAAACCAT 693  
Qy 667 CGGACCCACCCAGCAGCAGCGCGGCTTGAAGAACGACCTGCTGAGAACCTGCAGGC 726  
Db 694 TGGGACTCATCTAGCTCCAGTGTGCTGTAATAAATGCTCTTCTTGAATAATTTGCAGGC 753  
Qy 727 CTACCAGAAGCGCATGGGCTGCAGATGCAGCGCTTCAAGTGAAC 771  
Db 754 CTATCAGAAAGAAATGGGGTGCAGATGCACAGGTTCAAGTGATC 798

RESULT 7

US-09-506-286B-4  
; Sequence 4, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; APPLICANT: The University of Pittsburgh, of the Commonwealth  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
US-09-506-286B-4

Query Match 62.5%; Score 484.6; DB 3; Length 1023;  
Best Local Similarity 76.8%; Pred. No. 5.9e-83;  
Matches 592; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 1 AGATCTAAAGATGAGCTGCTGACCGAGGTGGAGACCTAGCTGCTGAGCATCATCCCCAG 60  
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGCGAAACGTAGCTTCTCTATCTTACCATC 74  
Qy 61 CGGCCCCCTGAAGCCCGAGATCGCCAGAGGCTGGAGGAGCTGTTCCGCGCAAGAACAC 120  
Db 75 AGGCCCCCTCAAGCCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCAGGAGAACAC 134  
Qy 121 CGACTCGAGGTGCTGATGAGTGGCTGAAGACAGGCCCCATCTGAGCCCCCTGACCAA 180  
Db 135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTCTGACCTCTGACTAA 194  
Qy 181 GGGCATCTGGGCTTCGTGTTCACTGACCGTCCCGAGGAGCGCGCTGACGCGCG 240  
Db 195 AGGATTTTAGGATTCGTATTCACGCTCACCGTCCCGAGGAGCTGACGAGCTAG 254  
Qy 241 CCGCTTCTGTCAGAAACCGCCCTGAAACCGCAACCGCGACCCCAACAACATGGAAGGCGGT 300  
Db 255 ACGTTTGTCCAAATGCCCCCTTAGTGAACCGGAGATCCAAACAACATGACAGAGCAGT 314  
Qy 301 GAAGCTGTACAGGAAGCTGAAGGGAGATCACTTCCAGCGCCCAAGGAGATCAGCCT 360  
Db 315 AAAACTGTACAGGAAGCTTAAAGAGAAATAACATTCATCGGGGCAAAAGAGGTGGCACT 374

Qy 361 GAGCTACAGCGCGCGCCCTGGCCAGCTGATGGGCTGTATCTAACAGGATGGCGC 420  
| | | | |  
Db 375 CAGCTATTCCACTGGTGCACCTAGCCAGCTGATGGGACTCATATACACAGAATGGGAAC 434  
| | | | |  
Qy 421 CGTGACACCGAGTGGCCCTTCGGCCCTGGTGTGCGCCACCTGGCAGCAGATCGCCGACAG 480  
| | | | |  
Db 435 TGTGACAAACGAAAGTGGCAATTTGGCCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494  
| | | | |  
Qy 481 CCAGCACCGCAGCCACAGGAGATGGTGACCCACCAACCAACCCCTGTATAGGCGACAGAA 540  
| | | | |  
Db 495 CCAGCATCGATCTCACAGGAGATGGTGACAAATACCAACCAATTAATCAGACATGAATA 554  
| | | | |  
Qy 541 CAGATGGTGTGGCCAGACACACCGCAAGGCCATGGAGCAGATGGCCGCGCAGACGGA 600  
| | | | |  
Db 555 CAGAAATGGTATTAGCCAGTACACCGGCTAAAGCCATGGAGCAGATGGCGGGTCCAGTGA 614  
| | | | |  
Qy 601 GCAGGCGCGAGGCCATGGAGTGGCCAGCCAGCCAGGCGAGATGGTGAGGCCCATGAG 660  
| | | | |  
Db 615 GCAGGCGAGAGAGGCCATGGAGTGGTGTAGTAGGCTAGGCGAGATGGTACAGGCAATGAG 674  
| | | | |  
Qy 661 GACCATCGGACACCAACCCAGCAGCGCGGCTGAAAGAACCAACCTGTGTGAGAACT 720  
| | | | |  
Db 675 AACCATTTGGGACCAACCTAGCTCCAGTGCGGGTTTGAAGATGATCTCCTTGAATTT 734  
| | | | |  
Qy 721 GCAGGCTACAGAAAGCCATGGCGTGCAGATGACGCGCTTCAAGTGAAC 771  
| | | | |  
Db 735 GCAGGCTACAGAAACGGATGGGAGTGCMAATGCAGCGATTCAAGTGATC 785  
| | | | |

## RESULT 8

US-09-762-861B-4  
; Sequence 4, Application US/09762861B  
; Patent No. 6579528  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS (formerly HK2-033CPUS)  
; CURRENT APPLICATION NUMBER: US/09/762,861B  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION:  
US-09-762-861B-4

Query Match 62.5%; Score 484.6; DB 3; Length 1023;  
Best Local Similarity 76.8%; Pred. No. 5.9e-83;  
Matches 592; Conservative 0; Mismatches 179; Indels 0; Gaps 0;  
Qy 1 AGATCTAAAGATGAGCTGTGACCGAGGTGGAGACCTACGTGTGATGAGCATCATCCCCAG 60  
| | | | |  
Db 15 ATATTTAAAGATGATCTTCTGACCGAGGTGGAACGTACGTTCTCTATCTTACCATC 74  
| | | | |  
Qy 61 CGGCCCCCTGAAGCCGAGATGGCCAGAGCTGGAGGACGTGTTGCGCGGCAAGAACAC 120  
| | | | |  
Db 75 AGGCCCCCTCAAGACCGAGATCGCGCAGAGACTTGAAGATGCTTTTGCAGGGGAAGAAC 134  
| | | | |  
Qy 121 CGACTGGAGTGTGATGGAGTGGCTGAAGACCAAGGCCATCTGAGCCCCCTGACCAA 180  
| | | | |

Db 135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACTCTGACTAA 194  
| | | | |  
Qy 181 GGGCATCTCTGGGCTTCTGTGTTCACTGACCTGCGGCCAGGAGCGGGCTCTGAGCGCCG 240  
| | | | |  
Db 195 AGGGATTTTAGGATTCGTATTCACTGCTCACCGTGGCCAGTGAAGGAGTGGAGCGTAG 254  
| | | | |  
Qy 241 CCGCTTCGTGCAGAACGCGCTGAAACGSCAACGCGCACCCCAACAAATGAGCAAGGCCGT 300  
| | | | |  
Db 255 ACCTTTTGTCCAAATGCGCTTAGTGAACAGGAGATCCAAACAACATGACAGAGCAGT 314  
| | | | |  
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACTTTCCACGGGCGCAAGAGATCAGCCT 360  
| | | | |  
Db 315 AAACTGTACAGGAAGCTTAAAGAGAAATAACATTCCATGGGCGCAAAAGAGTGGCACT 374  
| | | | |  
Qy 361 GAGCTACAGGCGCGGCGCCCTGGCCAGCTGCATGGGCTGTATCTAACAGGATGGCGGC 420  
| | | | |  
Db 375 CAGCTATTCCACTGGTGCACCTAGCCAGCTGCTAGGGAATCATATACAAAGAATGGGAAC 434  
| | | | |  
Qy 421 CGTGACACCGAGGTGGCCCTTCGGCTGTGTCGCCACCTGCGAGCAGATCGCCGACAG 480  
| | | | |  
Db 435 TGTGACAAACCGAAGTGGCATTTGGCCCTGGTATGGCCCAATGTGAACAGATCGCTGATTC 494  
| | | | |  
Qy 481 CCAGCACCGCAGCCACAGGAGATGGTGACCAACCAACCCCTGTATCAGGCGACGAA 540  
| | | | |  
Db 495 CCAGCATCGATCTCAAGGAGATGGTGACAAATAACCAATTAATCAGACATGAATA 554  
| | | | |  
Qy 541 CAGATGGTGTCTGGCCAGCACACCGCCAAAGGCCATGGAGCAGATGGCCGCGCAGCAGGA 600  
| | | | |  
Db 555 CAGAAATGGTATTAGCCAGTACCAAGCTAAAGCCATGGAGCAGATGGCGGGTCCAGTGA 614  
| | | | |  
Qy 601 GCAGGCGCGAGGCCATGGAGTGGCCAGCCAGGCGCGAGCAGATGGTGAGGCCCATGAG 660  
| | | | |  
Db 615 GCAGGCGAGAGAGGCCATGGAGTGGTGTAGTAGGCTAGGCGAGATGGTACAGGCAATGAG 674  
| | | | |  
Qy 661 GACCATCGGACACCAACCCAGCAGCGCGGCTGAAAGAACCAACCCCTGTATCAGGCGACCT 720  
| | | | |  
Db 675 AACCATTTGGGACCAACCTAGCTCCAGTGCGGGTTTGAAGATGATCTCCTTGAATTT 734  
| | | | |  
Qy 721 GCAGGCTACAGAAAGCCATGGCGTGCAGATGACGCGCTTCAAGTGAAC 771  
| | | | |  
Db 735 GCAGGCTACAGAAACGGATGGGAGTGCMAATGCAGCGATTCAAGTGATC 785  
| | | | |

## RESULT 9

US-10-065-133A-4  
; Sequence 4, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION:  
US-10-065-133A-4

Query Match 62.5%; Score 484.6; DB 3; Length 1023;  
Best Local Similarity 76.8%; Pred. No. 5.9e-83;  
Matches 592; Conservative 0; Mismatches 179; Indels 0; Gaps 0;



```
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert W.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
; OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
; OTHER INFORMATION: influenza matrix protein gene
; NAME/KEY: CDS
; LOCATION: (16)...(816)
; OTHER INFORMATION: PADRE-Influenza matrix
; US-09-311-784A-13

Query Match      61.6%; Score 477.4; DB 3; Length 816;
Best Local Similarity 76.8%; Pred. No. 1.3e-81;
Matches 583; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

Qy 11 ATGAGCTGTGACCGAGGTGGAGACCTACGTGTGTGAGCATCATCCCGAGCGGCCCTCG 70
Db 58 ATGAGTCTTAAACCGAGGTGGAACGTACGTCTCTCTATCATCCATCAGGCCCTC 117

Qy 71 AAGCCGAGATCGCCGAGAGGTGGAGACGTGTTCGCCGCGCAAGAACACCGACCTGGAG 130
Db 118 AAGCCGAGATCGCCGAGAGCTTGGAGATGTTTTCGAGGGAAGAACACAGATCTTGAG 177

Qy 131 GTGCTGATGAGTGTGCTGAAGACCAAGCCCATCTGTGAGCCCTTGAACCAAGGGATCTG 190
Db 178 GCTCTCATGGAATGCTTAAGACAAAGACCAATCTCTGTCACTTGAATGAAGGAATTTTA 237

Qy 191 GGCTTGTGTTTCACTTCAACCGTGCAGCGAGCGCGCTTGCAGCGCGCGCTTCTGTG 250
Db 238 GGGTTGTGTTTCACTTCAACCGTGCAGCGAGCGAGCTGCAGCGTAGACGATTTGTC 297

Qy 251 CAGAACCGCTGAACGGCAACCGCGACCCCAACATGGAACAGGCCGCTGAAGCTGTAC 310
Db 298 CAAATATGCCCTAAATGGGAATGGAGACCCCAACCAACATGGAACAGGCCGATTAACATATAC 357

Qy 311 AGGAAGCTGAAGAGGGAGATCACTTCCACGCGCCCAAGGAGATCAGCGCTGACGTACAGC 370
Db 358 AAGAACTGAAGAGGGAATGACATTCCTAGAGCAAGGAAGTTGCACTCAGTTACTCA 417

Qy 371 GCCGCGCCCTGGCAGCTGATGGGCTGTATCTAACACAGAGTGGCGCGCTGACCAACC 430
Db 418 ACTGGTGGCTTGGCAGTTGCATGGGTCTCATATACACCGGATGGGAACAGTGACCA 477

Qy 431 GAGTGGCTTGGCCTGGTGTGCGCCACTTGTGAGAGAGATCGCGCAGCGAGCACCGC 490
Db 478 GAAGTGGCTTGGCCTAGTATGTGCGCACTTGTGAGCAGATTTGCTGATGGCCCAACATCG 537

Qy 491 AGCCACAGGAGATGGTGCACCAACCAACCCCTGATCAGGCAAGCAAGAGATGGT 550
Db 538 TCCACAGGAGATGGGCACTTACCAACCAACCACTAATCAGGCAAGCAAGATGGTA 597

Qy 551 CTGGCAGCACCAACCGCAAGGCCATGGAGCAGATGGCGCGCAGCAGCAGCGCC 610
Db 598 CTAGCAGCACTACGGCTAAGGCCATGGAGCAATGGCTGGATCAAGTGAAGCAGCAGCA 657

Qy 611 GAGGCCATGGAAGTGGCGAGCCAGGCGCAGGATGGTGTGAGGCCATCAGGACCATCGCC 670
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Db 658 GAGCCATGAAGTGCAGATCAGGCTAGACAATGTGCGGCAATGAGCAATTTGGG 717
Qy 671 ACCCACCAGCAGCAGCGCGCTTGAAGAACGACCTCTGTGAGAACCTTGCAGGCTAC 730
Db 718 ACTCACCCTAGCTCCAGTGCAGGTCTAAAGATGATCTTATTGAAAATTTTCAGGCTTAC 777
Qy 731 CAGAAGCGCATGGCGTGTGAGATGAGCGCTTCAAGTGA 769
Db 778 CAGAAACCGATGGGGTGCAGATGCAGCGATTCAAGTGA 816

RESULT 12
US-09-506-286B-3
; Sequence 3, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; US-09-506-286B-3
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Query Match      51.6%; Score 477.2; DB 3; Length 756;
Best Local Similarity 76.9%; Pred. No. 1.4e-81;
Matches 581; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

Qy 11 ATGAGCTGTGACCGAGGTGGAGACCTACGTGTGTGAGCATCATCCCGAGCGGCCCTCG 70
Db 1 ATGAGTCTTCTGACCGAGGTGGAACGTACGTCTCTCTATCGTACCATCAGGCCCTC 60

Qy 71 AAGCCGAGATCGCCGAGAGGTGGAGACGTGTTCGCCGCGCAAGAACACCGACCTGGAG 130
Db 61 AAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGAGGGAAGAACACCGATCTTGAG 120

Qy 131 GTGCTGATGAGTGGCTGAAGACCAAGCCCATCTGTGAGCCCTTGAACCAAGGGATCTCG 190
Db 121 GCACTCATGGAATGGCTAAAGACAAAGACCAATCTCTGTCACTTGAATGAAGGAATTTTA 180

Qy 191 GGCTTGTGTTTCACTTCAACCGTGCAGCGAGCGCGCTTGCAGCGCGCGCTTCTGTG 250
Db 181 GGATTCGTATTACGCTCAGCGTGCAGCGCGAGGAGACTGTCAGCGCTGAGCGCTTGTGTC 240

Qy 251 CAGAACCGCTTGAACCGCAACCGCGACCCCAACAAATGGAACAAAGCGGTGAAGCTGTAC 310
Db 241 CAAATATGCCCTTGTGGAACCGGAGATCCAAACAAATGGAACAGAGAGAGTAAATCTGTAC 300

Qy 311 AGGAAGCTGAAGAGGGAGATCAGCTTCCAGCGCGCCAGGAGATCAGCGCTGAGCTACAGC 370
Db 301 AGGAAGCTTAAAGAGAGAAATAACATTCATGGGGCAAAAGAGGTGGCACTCAGCTATTTC 360

Qy 371 GCCCGCCCTTGGCAGCTGATGGGCTGTATCTTACAAACAGGATGGGCGCGCTGACCAACC 430
Db 361 ACTGGTGCATAGCAGCTGCATGGGACTCATATACAAAGATGGGAATCTGTGACACACC 420

Qy 431 GAGTGGCTTGGCCTGGTGTGCGCCACTTGTGAGCAGATTCGCCGAGCAGCAGCAGCGCC 490
Db 421 GAAGTGGCTTGGCCTGGTATGGCCACATGTGAACAGATCGCTGTGATTCAGCATCGA 480

Qy 491 AGCCACAGGAGATGGTGTGACCAACCAACCCCTGATCAGGCGAGAGAACAGGATGGT 550
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Db 481 TCTCAGGCGAGTGGTGAACAACCAACCCATTAATCAGACATGAATAACAGAAATGTA 540  
Qy 551 CTGGCCAGCACACCGCCCAAGCCATGAGCAGATGGCGCGCAGCAGCAGCCGCC 610  
Db 541 TTAGCCAGTACACCGCTAAAGCCATGAGCAGATGGCAGGGTTCGAGTGACGACGA 600  
Qy 611 GAGGCCATGGAGTGGCCAGCAGCCAGCAGGAGATGGTGCAGGCCATGAGCAGCAGCCG 670  
Db 601 GAGGCCATGGAGTGGTCTAGTAAGGCTAGGCGATGGTTCAGGCAATGAGAACCAATTGG 660  
Qy 671 ACCCAACCCAGCAGCAGCCCGCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCCTAC 730  
Db 661 ACCCAACCCAGCAGCAGCCCGCTTGAAGAGATGATCTCTTGAATAATTTCAGGCCCTAC 720  
Qy 731 CAGAGCCGATGGCGCTGCAGATGCGAGCTTCAAG 766  
Db 721 CAGAAACGGATGGGAGTGCAATGCAAGGATTCAAG 756

## RESULT 13

US-09-762-861B-3  
; Sequence 3, Application US/09762861B  
; Patent No. 6579528  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)  
; CURRENT APPLICATION NUMBER: US/09/762,861B  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-09-762-861B-3

Query Match 61.6%; Score 477.2; DB 3; Length 756;  
Best Local Similarity 76.9%; Pred. No. 1.4e-81;  
Matches 581; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

Qy 11 ATGAGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGCCCTG 70  
Db 1 ATGAGCTCTTCTGACCGAGGTGAAACGTACGTCTCTCTATCTGATCAATCAGGCCCTC 60  
Qy 71 AAGGCCGAGATCGCCAGAGGCTGGAGGACGTGTTCCGCGCAAGAACACCGACCTGGAG 130  
Db 61 AAGGCCGAGATCGCCAGAGGCTGGAAGATGCTTTGCGGGAAGAACACCGATCTTGAG 120  
Qy 131 GTGCTGATGGATGGCTGAAGACCAAGCCCATCTCGAGCCCTTGACCAAGGGCATCTG 190  
Db 121 GCACCTCATGGAATGGCTAAAGACCAACCAATCTCTCTATCTGATCAATGAGGGATTTTA 180  
Qy 191 GGCTTCGTGTTACCTTGCAGCGTCCCGAGCGCGCTGCGAGCGCGCGCTTCGTCG 250  
Db 181 GGATTCGTATTACCTCTCAGCTCAGCTGCGGAGGACTGCGAGCTAGACGCTTTGTC 240  
Qy 251 CAGAACGCCCTGAACCGCAACGGCCACCCCAACATGAGCGCGCTGAAGCTGTAC 310  
Db 241 CAARATGCCCTTAGTGGAAACGGAGATCCAAACACATGGACAGACGATGAACCTGTAC 300  
Qy 311 AGGAAGCTGAAGAGGGAGATCACTTTCCAGCGGCCAAGAGGATCAGCTGAGCTACAGC 370  
Db 301 AGGAAGCTTAAAGAGAAATAACATTCATGGGCAAGAGAGGTGGCACTCAGCTATTTC 360

Qy 371 GCCGCGCCCTGGCAGCTGCATGGGCTGATCTTACAACAGATGGCGCGCTGACCAACC 430  
Db 361 ACTGGTGCATCTAGCCAGCTGCATGGGACTCATATAACAAGATGGGAACCTGTGACACC 420  
Qy 431 GAGTGGCTTTCGCGCTTGGTGGCCACCTGCGAGCAGATGCGCGCAGCAGCAGCAGCCGC 490  
Db 421 GAACTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCCGACATCGA 480  
Qy 491 AGCCACAGGCGAGATGGTGACCACCAACCCCTGATCAGGCGACGAGAACAGGATGGT 550  
Db 481 TCTCAGAGGCGATGGTGAACAACCAACCAACCATTAATCAGACATGAACAAGATGTA 540  
Qy 551 CTGGCCAGCACACCGCCAAAGGCCATGGAGCAGATGGCGCGCAGCAGCAGCAGCCGCC 610  
Db 541 TTAGCCAGTACACCGCTAAAGCCATGGAGCAGATGGCAGGCTCGAGTGGAGCAGCAGCA 600  
Qy 611 GAGGCCATGGAGTGGCGCAGCCAGCGCAGGAGATGGTGCAGGCCATGAGAACCATCGGC 670  
Db 601 GAGGCCATGGAGTGGCTAGTAAGGCTAGGCGGTTTGAAGAGATGCTCTTGAATAATTTCAGGCCCTAC 720  
Qy 671 ACCCAACCCAGCAGCAGCGCGCTTGAAGAACACCACTGCTGGAGAACCTTCAGGCCCTAC 730  
Db 661 ACCCAACCCAGCAGCAGCGGTTTGAAGAGATGATCTCTTGAATAATTTCAGGCCCTAC 720  
Qy 731 CAGAAACGGATGGGAGTGCAATGCAAGGATTCAAG 766  
Db 721 CAGAAACGGATGGGAGTGCAATGCAAGGATTCAAG 756

## RESULT 14

US-10-065-133A-3  
; Sequence 3, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-3

Query Match 61.6%; Score 477.2; DB 3; Length 756;  
Best Local Similarity 76.9%; Pred. No. 1.4e-81;  
Matches 581; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

Qy 11 ATGAGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGCCCTG 70  
Db 1 ATGAGCTCTTCTGACCGAGGTGAAACGTACGTCTCTCTATCTGATCAATGAGGGCTC 60  
Qy 71 AAGGCCGAGATCGCCAGAGGCTGGAGGACGTGTTCCGCGCAAGAACACCGACCTGGAG 130  
Db 61 AAGGCCGAGATCGCCAGAGGCTTGAAGATGCTTTGCGGGAAGAACACCGATCTTGAG 120  
Qy 131 GTGCTGATGGATGGCTGAAGACCAAGCCCATCTCGAGCCCTTGACCAAGGGCATCTG 190  
Db 121 GCACCTCATGGAATGGCTAAAGACCAACCAATCTCTCTATCTGATCAATGAGGGATTTTA 180  
Qy 191 GGCTTCGTGTTACCTTGCAGCGTCCCGAGCGCGCTGCGAGCGCGCGCTTCGTCG 250  
Db 181 GGATTCGTATTACCTCTCAGCTCAGCTGCGGAGGACTGCGAGCTAGACGCTTTGTC 240  
Qy 251 CAGAAACGCCCTGAACCGCAACGGCGGCCCAACCAACATGAGCGCGCTGAAGCTGTAC 310

Db 241 CAAATGCCCTTAGTGGAAACGGAGATCCAAACACATGGACAGAGCAGTAAACTGTAC 300  
Qy 311 AGGAAGCTGAAGAGGAGATCACCTTCCACGGCCCAAGGAGATCAGCCTGAGCTACAGC 370  
Db 301 AGGAGCTTAAAGAGAAATAACATTCCATGGGGCNAAGAGGTGGCACTCAGCTATTCC 360  
Qy 371 GCGGCGCCCTGGCCAGCTGCATGGGCTTGATCTACCAAGGATGGGGCGGTGACCAACC 430  
Db 361 ACTGGTGCATAGCCAGCTGCATGGGACTCATATACCAAGATGGGAATCTGTGACAACC 420  
Qy 431 GAGTGGCCCTTCGGCCTGGTGGCCACCTGCGAGCAGATCGCCGACGCCAGCACGGC 490  
Db 421 GAAGTGGCATTTGGCCCTGGTATGGCCACATGTGAACAGATCGCTGATTTCCAGCATCGA 480  
Qy 491 AGCCACAGGAGATGGTGACCAACCAACCCCTGATCAGGCACGAGAACAGAGATGGTG 550  
Db 481 TCTCAGAGGAGATGGTGACCAACCAACCCATTAATCAGACATGAACAGATGGTA 540  
Qy 551 CTGCGCAGCACCAACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCGCCGCC 610  
Db 541 TTAGCCAGTACCAACCGCTTAAAGCCATGGAGCAGATGGCAGGTGCGAGTGAAGCAGCA 600  
Qy 611 GAGCCATGAGGTGGCCAGCCAGCCAGCAGATGGTGGCCATGAGGACCATCGCC 670  
Db 601 GAGCCATGAGGTGGTGTAGTAAGGCTAGGAGATGGTTCAGGCAATGAGAACCATTGGG 660  
Qy 671 ACCCACCAGCAGCAGCGCGCTGAAGAACGACCTGCTGGAGAACCTGCGAGGCCCTAC 730  
Db 661 ACCCACCAGTCTCAGTGGCGGTTGAAAGATGATCTCTTGAATTTGCGAGGCCCTAC 720  
Qy 731 CAGAAAGCGCATGGCGCTGCAGATCGAGCTTCAAG 766  
Db 721 CAGAAACGATGGGAGTGCAATGCAGCGATTCAAG 756

## RESULT 15

US-10-434-811A-3  
; Sequence 3, Application US/10434811A  
; Patent No. 6824784  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; Education  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-CL-PUS-1  
; CURRENT APPLICATION NUMBER: US/10/434,811A  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-434-811A-3

Query Match 61.6%; Score 477.2; DB 3; Length 756;  
Best Local Similarity 76.9%; Pred. No. 1.4e-81;  
Matches 581; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

Qy 11 ATGAGCCTGTGACCGAGGTGGAGACCTACGTGTGACGATCATCCCCAGCGGCCCTTG 70  
Db 1 ATGAGTCTTCTGACCGAGGTGGAACGATACGTCTCTATCGTACCATCAGGCCCTC 60  
Qy 71 AAGGCCGAGATCGCCAGAGGCTGGAGGACGTGTTCGCGGCAAGAACCCGACCTGGAG 130  
Db 61 AAAGCCGAGATCGCCAGAGACTTGAAGATGTCCTTTCAGGGAGAGAACCCGATCTTGAG 120

Qy 131 GTCTGATGAGTGGCTGAAGACAGGCCCATCTGAGCCCTGACCAAGGSCATCTG 190  
Db 121 GCATCATGAATGGCTTAAAGACAAGACCAATCTGTACCTCTGACTTAAGGATTTTA 180  
Qy 191 GGCCTTGGTTCACCTTCAGCCGTGCGCCAGCGAGCGGCTGCGAGCGCCGCTTGGTG 250  
Db 181 GGATTGGTATTCAAGCTCACCGTGCCTGAGGAGGACTGCGAGCGTACGACTTTGTC 240  
Qy 251 CAGAAAGCCCTGAAACGGCGAACCGCGACCCCAACAAATGGACAAAGCCGTGAAGCTGTAC 310  
Db 241 CAAATATGCCCTTAGTGGAAACCGGAGATCCAAACAAATGACAGAGCAGTAAACTGTAC 300  
Qy 311 AGGAAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGGAGATCAGCCTGAGCTACAGC 370  
Db 301 AGGAAGCTTAAAGAGAAATAACATTCCATGGGGCAAAAGAGTGGCACTCAGCTATTCC 360  
Qy 371 GCGCGGCCCTGCGCCAGCTGTCATGGGCTGATCTACAAAGGATGGGCGCGGTGACCAACC 430  
Db 361 ACTGGTGCATGACCGAGCTGCTGGGACTCATATACAAAGATGGGAACTGTGACAACC 420  
Qy 431 GAGGTGGCTTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCAGCACCGC 490  
Db 421 GAAGTGGCATTTTGGCCTGGTATGCGCCACATGTGTAACAGATCGCTGATTTCCAGCATCGA 480  
Qy 491 AGCCACAGGCGAGTGGTGACCAACCAACCCCTGATCAGGCAACGAGACAGATGGTG 550  
Db 481 TCTCAGAGGAGATGGTGACCAACCAACCCCATTAATCAGACATGAACAGATGGTA 540  
Qy 551 CTGCGCAGCACCAACCGCCAGGCGCATGGAGCAGATGGCCGCGCAGCAGCGAGCGGCC 610  
Db 541 TTAGCCAGTACCAACCGCTTAAAGCCATGGAGCAGATGGCAGGTGCGAGTGAAGCAGCA 600  
Qy 611 GAGGCCATGAGTGGCGCCAGCCAGGCGCAGCAGATGGTGCAGGCGATGAGGACCATCGGC 670  
Db 601 GAGGCCATGAGGTGCTAGTAAGGCTAGGCGAGATGGTTCAGGCAATGAGAACCATTGGG 660  
Qy 671 ACCCACCAGCAGCAGCGCGCTGAAGAACGACCTGCTGGAGAACCTGCGAGGCCCTAC 730  
Db 661 ACCCACCAGTCTCAGTGGCGGTTTGAAGATGATCTCTTGAATTTGCGAGGCCCTAC 720  
Qy 731 CAGAAAGCGCATGGCGCTGCAGATCGAGCGCTTCAAG 766  
Db 721 CAGAAACGATGGGAGTGCAATGCAGCGATTCAAG 756

Search completed: March 20, 2006, 23:50:21

Job time : 159.134 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:29:50 ; Search time 761.784 Seconds  
(without alignments)  
8412.838 Million cell updates/sec

Title: US-10-729-830-3  
Perfect score: 775  
Sequence: 1 agactaaagatgagctgc.....agcggtcaagtgaactagt 775

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:\*

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6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

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9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description      |
|------------|-------|-------------|--------|-------|------------------|
| 1          | 775   | 100.0       | 775    | 8     | US-10-729-830-3  |
| 2          | 775   | 100.0       | 942    | 8     | US-10-729-830-6  |
| 3          | 762   | 98.3        | 844    | 8     | US-10-729-830-4  |
| 4          | 762   | 98.3        | 1011   | 8     | US-10-729-830-7  |
| 5          | 499.8 | 64.5        | 942    | 8     | US-10-729-830-5  |
| 6          | 498.8 | 64.4        | 774    | 8     | US-10-729-830-1  |
| 7          | 497   | 64.1        | 985    | 8     | US-10-855-484-9  |
| 8          | 489.4 | 63.1        | 1027   | 6     | US-10-177-390-31 |
| 9          | 487.4 | 62.9        | 1023   | 6     | US-10-065-133A-1 |
| 10         | 487.4 | 62.9        | 1023   | 7     | US-10-434-811A-1 |
| 11         | 487.4 | 62.9        | 1023   | 7     | US-10-734-373-1  |
| 12         | 487.4 | 62.9        | 1023   | 8     | US-10-872-014-1  |
| 13         | 486.2 | 62.9        | 1027   | 8     | US-10-855-875-5  |
| 14         | 484.6 | 62.5        | 1023   | 6     | US-10-065-133A-4 |
| 15         | 484.6 | 62.5        | 1023   | 7     | US-10-434-811A-4 |
| 16         | 484.6 | 62.5        | 1023   | 7     | US-10-734-373-4  |
| 17         | 484.6 | 62.5        | 1023   | 8     | US-10-872-014-4  |
| 18         | 477.4 | 61.6        | 816    | 6     | US-10-371-525-13 |
| 19         | 477.4 | 61.6        | 816    | 6     | US-10-371-069-13 |
| 20         | 477.4 | 61.6        | 816    | 6     | US-10-371-645-13 |
| 21         | 477.4 | 61.6        | 816    | 6     | US-10-371-260-13 |
| 22         | 477.2 | 61.6        | 756    | 6     | US-10-065-133A-3 |
| 23         | 477.2 | 61.6        | 756    | 7     | US-10-434-811A-3 |

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|----|-------|------|------|---|--------------------|--------------------|
| 24 | 477.2 | 61.6 | 756  | 7 | US-10-734-373-3    | Sequence 3, Appli  |
| 25 | 477.2 | 61.6 | 756  | 8 | US-10-872-014-3    | Sequence 3, Appli  |
| 26 | 474.6 | 61.2 | 1002 | 3 | US-09-747-335-3    | Sequence 3, Appli  |
| 27 | 474.6 | 61.2 | 1002 | 7 | US-10-435-723A-3   | Sequence 3, Appli  |
| 28 | 474.4 | 61.2 | 756  | 6 | US-10-065-133A-6   | Sequence 6, Appli  |
| 29 | 474.4 | 61.2 | 756  | 7 | US-10-434-811A-6   | Sequence 6, Appli  |
| 30 | 474.4 | 61.2 | 756  | 7 | US-10-734-373-6    | Sequence 6, Appli  |
| 31 | 474.4 | 61.2 | 756  | 8 | US-10-872-014-6    | Sequence 6, Appli  |
| 32 | 473.4 | 61.1 | 1027 | 7 | US-10-381-530-7    | Sequence 7, Appli  |
| 33 | 472.6 | 61.0 | 759  | 8 | US-10-617-569-3    | Sequence 3, Appli  |
| 34 | 77.6  | 10.0 | 1092 | 6 | US-10-138-098-13   | Sequence 13, Appli |
| 35 | 77.6  | 10.0 | 1092 | 8 | US-10-476-615-13   | Sequence 13, Appli |
| 36 | 77.6  | 10.0 | 3020 | 6 | US-10-138-098-21   | Sequence 21, Appli |
| 37 | 77.6  | 10.0 | 3020 | 8 | US-10-476-615-21   | Sequence 21, Appli |
| 38 | 77.6  | 10.0 | 3021 | 6 | US-10-138-098-22   | Sequence 22, Appli |
| 39 | 77.6  | 10.0 | 3021 | 6 | US-10-138-098-23   | Sequence 23, Appli |
| 40 | 77.6  | 10.0 | 3021 | 6 | US-10-138-098-24   | Sequence 24, Appli |
| 41 | 77.6  | 10.0 | 3021 | 8 | US-10-476-615-22   | Sequence 22, Appli |
| 42 | 77.6  | 10.0 | 3021 | 8 | US-10-476-615-23   | Sequence 23, Appli |
| 43 | 77.6  | 10.0 | 3021 | 8 | US-10-476-615-24   | Sequence 24, Appli |
| 44 | 77    | 9.9  | 1377 | 8 | US-10-411-910A-266 | Sequence 266, App  |
| 45 | 76.2  | 9.8  | 1725 | 8 | US-10-411-910A-196 | Sequence 196, App  |

ALIGNMENTS

RESULT 1

US-10-729-830-3

; Sequence 3, Application US/10729830

; Publication No. US20050032730A1

; GENERAL INFORMATION:

; APPLICANT: Von der Muelbe, Florian

; APPLICANT: Hoert, Ingmar

; APPLICANT: Pascoco, Steve

; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA

; TITLE OF INVENTION: Optimised for translation in its coding regions

; FILE REFERENCE: 2793-1-001PCT/CIP

; CURRENT APPLICATION NUMBER: US/10729,830

; CURRENT FILING DATE: 2003-12-05

; PRIOR APPLICATION NUMBER: PCT/EP02/06180

; PRIOR FILING DATE: 2002-06-05

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; TYPE: DNA

; LENGTH: 775

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Influenza

; OTHER INFORMATION: matrix: gene with increased G/C-content

; FEATURE:

; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop

; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)

US-10-729-830-3

Query Match 100.0%; Score 775; DB 8; Length 775;

Best Local Similarity 100.0%; Pred. No. 8.3e-175; Indels 0; Gaps 0;

Matches 775; Conservative 0; Mismatches 0;

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| Qy | 1   | AGATCTAAAGATGAGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG | 60  |
| Db | 1   | AGATCTAAAGATGAGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG | 60  |
| Qy | 61  | CGSCCCCTGAAAGGCGAGATCCGCCAGAGCGGTGGAGAGCGTTCGCCCGGCAAGACAC  | 120 |
| Db | 61  | CGSCCCCTGAAAGGCGAGATCCGCCAGAGCGGTGGAGAGCGTTCGCCCGGCAAGACAC  | 120 |
| Qy | 121 | CGACCTGGAGGTGCTGATGGAGTGGTGAAGACAGCCCATCTGAGCCCCCTGACCAA    | 180 |
| Db | 121 | CGACCTGGAGGTGCTGATGGAGTGGTGAAGACAGCCCATCTGAGCCCCCTGACCAA    | 180 |
| Qy | 181 | GGGCATCTGGGCTTCGTGTTACCTGACCGTCCCGAGCGCGCGCTGCAGCGCG        | 240 |

Db 181 GGGCATCTGGGCTTCGTGTTACCTTGCACCTGACCTGCCAGGAGCGCGCTGCAGCGCCG 240  
Qy 241 CCGCTTCGTGAGAAAGCGCTTGAACGCAACGCGGACCGCCCAACAAATGACAAAGGCGGT 300  
Db 241 CCGCTTCGTGAGAAAGCGCTTGAACGCAACGCGGACCGCCCAACAAATGACAAAGGCGGT 300  
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACCTTCCACGGCGCCCAAGGAGATCAGCCT 360  
Db 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACCTTCCACGGCGCCCAAGGAGATCAGCCT 360  
Qy 361 GAGCTACAGCGCGCGCGCTTGGCCAGCTGATGGGCTGTATACAAAGGATGGCGC 420  
Db 361 GAGCTACAGCGCGCGCGCTTGGCCAGCTGATGGGCTGTATACAAAGGATGGCGC 420  
Qy 421 CGTGACCAACGAGGTGGCTTGGCCCTGGTGTGCGCCACCTTGCAGCAGATCGCGCAG 480  
Db 421 CGTGACCAACGAGGTGGCTTGGCCCTGGTGTGCGCCACCTTGCAGCAGATCGCGCAG 480  
Qy 481 CCAGCAGCGCAGCCACAGGAGATGGTGAACCAACCAACCCCTGTATAGGCAAGGAA 540  
Db 481 CCAGCAGCGCAGCCACAGGAGATGGTGAACCAACCAACCCCTGTATAGGCAAGGAA 540  
Qy 541 CAGATGGTGTGCGCAGCACCACCGCAAGGCCATGGAGCAGATGCGCGCAGCGGA 600  
Db 541 CAGATGGTGTGCGCAGCACCACCGCAAGGCCATGGAGCAGATGCGCGCAGCGGA 600  
Qy 601 GCAGGCGCGGAGGCGCATGGAGTGGCCAGCGCAGGCGCAGGAGTGTGAGGCGCATGAG 660  
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Qy 661 GACCATCGGCAACCCACCGCAGCAGCGCGCGCTGAAGAACGACCTTGTGAGAACT 720  
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RESULT 2  
US-10-729-830-6  
; Sequence 6, Application US/10729830  
; Publication No. US20050032730A1  
; GENERAL INFORMATION:  
; APPLICANT: Von der Muelbe, Florian  
; APPLICANT: Hoerr, Ingmar  
; APPLICANT: Pascolo, Steve  
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA  
; TITLE OF INVENTION: Optimised for translation in its coding regions  
; FILE REFERENCE: 2793-1-001PCT/CIP  
; CURRENT APPLICATION NUMBER: US/10/729,830  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: PCT/EP02/06180  
; PRIOR FILING DATE: 2002-06-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 942  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Influenza  
; OTHER INFORMATION: matrix: mRNA with increased G/C-content and  
; OTHER INFORMATION: stabilisation sequences  
; FEATURE:  
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-  
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,  
; OTHER INFORMATION: respectively.  
; FEATURE:  
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop  
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)  
US-10-729-830-6

Query Match 100.0%; Score 775; DB 8; Length 942;  
Best Local Similarity 87.7%; Pred. No. 8.3e-175;  
Matches 680; Conservative 95; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGATCTAAGATGAGCTGCTGACCGAGGTGGAGACCTAGCTGTAGCATCATCCCCAG 60  
Db 46 AGAUCUAAAGAGGCGCUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG 105  
Qy 61 CGGCCCCCTGAAGGCCGAGATCGCCACAGAGGCTGGAGAGCTGTTCGCCCGGCAAGAAC 120  
Db 106 CGGCCCCCTGAAGGCCGAGAUCCGCCAGAGCGUGGAGGACGUGUUCGCCGCAAGAAC 165  
Qy 121 CGACCTGGAGGTGCTGATGAGTGGTGAAGACAGGCCCATCTCTAGAGCCCCCTGACAA 180  
Db 166 CGACCUUGAGGUGCUGAUGGAGUGGUGGUGAAGACAGGCCCAUCCUGAGCCCCCAGCAA 225  
Qy 181 GGGCATCTGGGCTTGGTGTTCACCTGACCGTGGCCAGCGGCGCGCTGCAGCGCCG 240  
Db 226 GGGCAUCCUGGGCUUGUGUUACCCUGACCGUGGCCAGCGAGCGCGCCUGAGCGCCG 285  
Qy 241 CCGCTTCGTGCAGAAAGCCCTTGAAACGGCAACGGCGAACCCCAACAAATGGAAGGCGGT 300  
Db 286 CCGCUUGUGAGGACGAGCGCCUGAAGCGCAACGGCGAACCCCAACAAUGGAGGCGCGU 345  
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACTTCCACGGCGCCCAAGGAGATCAGCCT 360  
Db 346 GAAGCUGUACAGGAAGCUGAAGAGGGAGAUCAUCCUCCACGGCGCCCAAGGAGAUCAGCCU 405  
Qy 361 GAGCTACAGCGCGCGCGCTGCGCAGCTGCTAGTGGGCTGTATACAAAGGATGGCGC 420  
Db 406 GAGCUACAGCGCGCGCGCCUUGGCCAGCUGCAUGGGCCUGAUCAACAGGAUGGGCGC 465  
Qy 421 CGTGACCAACCGAGGTGGCTTTCGGCCCTGTGTGCGCCACCTTGCAGCAGATCGCGCAG 480  
Db 466 CGUGACCAACCGAGGUGGCCUUCGGCCUGUGUGGCCACCCUGCAGCAGAUCCCGCAG 525  
Qy 481 CCAGCAGCGCAGCCACAGGAGATGTTGAACACCAACCCCTGTATAGGAGCAGAGAA 540  
Db 526 CCAGCAGCGCAGCCACAGGAGAUUGUGAACACCAACCCCGCUGAUCAGGCAAGGAGAA 585  
Qy 541 CAGGATGGTGTGGCAGCACACCGCCAAAGGCCATGGAGCAGATGCGCGCAGCAGCGA 600  
Db 586 CAGGAUGGUGCUGGCCAGCACCCAGGCCCAUGGAGCAGAUCCCGCAGCAGCGA 645  
Qy 601 GCAGGCGCGCGAGCCATGGAGTGGCCAGCGCAGGCGCAGCAGATGTTGAGGCGCATGAG 660  
Db 646 GCAGGCGCGCGAGGCCCAUGGAGGUGGCCAGGCCAGGAGGUGGAGGCGCAUGAG 705  
Qy 661 GACCATCGGCAACCCACCGCCAGCAGCAGCGCGCGCTGAAGAACGACCTGTGAGGAGAACCT 720  
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Qy 721 GCAGGCTACCAAGAGCGCATGGGCGTGCAGATGCGAGCTTCAAGTGAACCTAGT 775  
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US-10-729-830-4  
; Sequence 4, Application US/10729830  
; Publication No. US20050032730A1  
; GENERAL INFORMATION:  
; APPLICANT: Von der Muelbe, Florian  
; APPLICANT: Hoerr, Ingmar  
; APPLICANT: Pascolo, Steve  
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA  
; TITLE OF INVENTION: Optimised for translation in its coding regions  
; FILE REFERENCE: 2793-1-001PCT/CIP  
; CURRENT APPLICATION NUMBER: US/10/729,830  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: PCT/EP02/06180  
; PRIOR FILING DATE: 2002-06-05

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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 844
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: gene for secreted form (with N-terminal
; OTHER INFORMATION: signal sequence) with increased G/C-content
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 836 to 838)
US-10-729-830-4

Query Match      98.3%; Score 762; DB 8; Length 844;
Best Local Similarity 100.0%; Pred. No. 1e-171;
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGGCCCTGAAG 73
Db 83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGGCCCTGAAG 142
Qy 74 GCCGAGATCGCCGAGGCTGGAGGACGTGTTCCGCCGCAAGAACACCGACCTGGAGGTG 133
Db 143 GCCGAGATCGCCGAGGCTGGAGGACGTGTTCCGCCGCAAGAACACCGACCTGGAGGTG 202
Qy 134 CTGATGGAGTGGCTGAAGACAGAGCCGATCTCTGAGCCGCTGACCAAGGGCATCTGGGC 193
Db 203 CTGATGGAGTGGCTGAAGACAGAGCCGATCTCTGAGCCGCTGACCAAGGGCATCTGGGC 262
Qy 194 TTGCTGTTTACCTGACCGTGCACGAGCGCGGCTTGCAGCGCGCGCTTGTGTGCGAG 253
Db 263 TTGCTGTTTACCTGACCGTGCACGAGCGCGGCTTGCAGCGCGCGCTTGTGTGCGAG 322
Qy 254 AACGCGCTTGAACGGCAACCGGCAACCCCAACAACTGGAACAAGGCGGTGAAGCTGTACAGG 313
Db 323 AACGCGCTTGAACGGCAACCGGCAACCCCAACAACTGGAACAAGGCGGTGAAGCTGTACAGG 382
Qy 314 AAGCTGAAGAGGAGATCACCTTCCAGCGCGGCAAGGAGATCAGGCTGAGCTACAGCGCC 373
Db 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCGGCAAGGAGATCAGGCTGAGCTACAGCGCC 442
Qy 374 GCGCGCTTGGCCAGCTGATGCGGCTGATCTACAAACAGATGGGCGGCTGACCAACCGAG 433
Db 443 GCGCGCTTGGCCAGCTGATGCGGCTGATCTACAAACAGATGGGCGGCTGACCAACCGAG 502
Qy 434 GTGGCCTTTCGGCTGGTGTGGCCACCTTCGAGCAGAGATCGCGCAGCAGCAGCAGCGCAGC 493
Db 503 GTGGCCTTTCGGCTGGTGTGGCCACCTTCGAGCAGAGATCGCGCAGCAGCAGCAGCGCAGC 562
Qy 494 CACAGGAGATGTTGACACACACACACCCCTGATCAGGCAAGAGAAAGAGATGTTGCTG 553
Db 563 CACAGGAGATGTTGACACACACACACCCCTGATCAGGCAAGAGAAAGAGATGTTGCTG 622
Qy 554 GCCAGCACCGCCCAAGGCCATGGAGCAGATGGCGGCGAGCAGGAGCAGCGCGCGCGAG 613
Db 623 GCCAGCACCGCCCAAGGCCATGGAGCAGATGGCGGCGAGCAGGAGCAGCGCGCGCGAG 682
Qy 614 GCCATGAGAGTGGCCAGCGCAGGAGGAGATGGTGTGAGGCGCATGAGGACCATCGGCAC 673
Db 683 GCCATGAGAGTGGCCAGCGCAGGAGGAGATGGTGTGAGGCGCATGAGGACCATCGGCAC 742
Qy 674 CACCCAGCAGCAGCGCGGCTGAAGAAACGACTGCTGGAGAACCTTCAGGCGCTTACAG 733
Db 743 CACCCAGCAGCAGCGCGGCTGAAGAAACGACTGCTGGAGAACCTTCAGGCGCTTACAG 802
Qy 734 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAGTACT 775
Db 803 AAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAGTACT 844
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US-10-729-830-7
; Sequence 7, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION: Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1011
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA coding for secreted form with
; OTHER INFORMATION: increased G/C-content and stabilisation sequences
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 881 to 883)
US-10-729-830-7

Query Match      98.3%; Score 762; DB 8; Length 1011;
Best Local Similarity 87.9%; Pred. No. 1e-171;
Matches 670; Conservative 92; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGGCCCTGAAG 73
Db 128 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGGCCCTGAAG 187
Qy 74 GCCGAGATCGCCGAGGCTGGAGGACGTGTTCCGCCGCAAGAACACCGACCTGGAGGTG 133
Db 188 GCCGAGATCGCCGAGGCTGGAGGACGTGTTCCGCCGCAAGAACACCGACCTGGAGGTG 247
Qy 134 CTGATGAGTGGCTGAAGACAGAGCGCCATCTCTGAGCGGCCCTTGAACAAGGGCATCTGGGC 193
Db 248 CUGAUGGAGUGGCUAGAAGACAGCGCCCAUCCUGAGCGCCCGCUGACCAAGGGCAUCCUGGCG 307
Qy 194 TTGCTGTTTACCTGACCGTGCAGCGCGGCTTGCAGCGCGCGCTTGTGTGCGAG 253
Db 308 TTGCTGTTTACCTGACCGTGCAGCGCGGCTTGCAGCGCGCGCTTGTGTGCGAG 367
Qy 254 AACGCGCTTGAACGGCAACCGGCAACCCCAACAACTGGAACAAGGCGGTGAAGCTGTACAGG 313
Db 368 AACGCGCTTGAACGGCAACCGGCAACCCCAACAACTGGAACAAGGCGGTGAAGCTGTACAGG 427
Qy 314 AAGCTGAAGAGGAGATCACCTTCCAGCGCGGCAAGGAGATCAGCCTGAGCTACAGCGCC 373
Db 428 AAGCTGAAGAGGAGATCACCTTCCAGCGCGGCAAGGAGATCAGCCTGAGCTACAGCGCC 487
Qy 374 GCGCGCTTTCGGCTGGTGTGGCCACCTTCGAGCAGAGATGGCGGCGAGCAGCGCGCGAG 433
Db 488 GCGCGCTTTCGGCTGGTGTGGCCACCTTCGAGCAGAGATGGCGGCGAGCAGCGCGCGAG 547
Qy 434 GTGGCCTTTCGGCTGGTGTGGCCACCTTCGAGCAGAGATGGCGGCGAGCAGCGCGCGAG 493
Db 548 GTGGCCTTTCGGCTGGTGTGGCCACCTTCGAGCAGAGATGGCGGCGAGCAGCGCGCGAG 607
Qy 494 CACAGGAGATGTTGACACACACACCCCTGATCAGGCAAGAGAAAGAGATGTTGCTG 553
Db 608 CACAGGAGATGTTGACACACACACCCCTGATCAGGCAAGAGAAAGAGATGTTGCTG 667
Qy 554 GCCAGCACCGCCCAAGGCCATGGAGCAGATGGCGGCGAGCAGGAGCAGCGCGCGCGAG 613
Db 668 GCCAGCACCGCCCAAGGCCATGGAGCAGATGGCGGCGAGCAGGAGCAGCGCGCGCGAG 727
```

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Qy 614 GCATGAGTGGCCAGCCAGCCAGGCGAGGATGTGTGAGGCGCATGAGGACCATCGGCACC 673
Db 728 GCCAUGAGGUGGCGAGCCAGCCAGGCGAGGCGAGGUGGCGCAUGAGGAGCCAUCCGCGACC 787
Qy 674 CACCCAGCAGCAGCGCGCGCTGAAGAACGACCTGTGTGAGAACCTGCGAGGCGCTACGAG 733
Db 788 CACCCAGCAGCAGCGCGCGCTGAAGAACGACCTGTGTGAGAACCTGCGAGGCGCTACGAG 847
Qy 734 AAGCGCATGGCGTGCAGATGCGAGCTTCAAGTGAACCTAGT 775
Db 848 AAGCGCAUGGCGGCGAGGAGCGGCUUCAAAGUAGAACUAGU 889

RESULT 5
US-10-729-830-5
; Sequence 5, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: Optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; PRIOR FILING DATE: 2003-12-05
; PRIOR FILING DATE: PCT/EP02/06180
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-5

Query Match 64.5%; Score 499.8; DB 8; Length 942;
Best Local Similarity 65.5%; Pred. No. 2.4e-109; Indels 0; Gaps 0;
Matches 508; Conservative 95; Mismatches 172;

Qy 1 AGATCTAAAGATGAGCCCTGTGACCGAGGTGGAGACCTTACGTGTGAGCATCATCCCCAG 60
Db 46 AGAUCUAAAGAUAGUCUUAUACCGAGUGGAAAGUAGUUCUUAUUAUUAUUAUUAUUAUUA 105
Qy 61 CGGCCCCCTGAAGCGCGAGATCGCCAGAGGCTGGAGACGTGTGTGCGCGCGAGAACAC 120
Db 106 AGGCCCCCTGAAGCGCGAGATCGCCAGAGGCTGGAGACGTGTGTGCGCGCGAGAACAC 165
Qy 121 CGACCTGGAGTGTGTGAGTGGCTGAAGACGAGGCGCCATCTGAGCGCCCTGACCAA 180
Db 166 CGAUCUUGAGGUGUUCUUAUGGAUUGGCUAAAGACAAAGACCAUCCUUGUACCCUUGACUA 225
Qy 181 GGGCATCTCGGGCTTCTGTGTTTCAACCTGACCGTGCACCGAGCGCGCGCTGCGAGCGCG 240
Db 226 GGGGAUUUAGGAUUUGUUAUACGUCUACCGUGGCCAGUGAGCGAGGACUGAGCGGUAG 285
Qy 241 CGGCTTGTGAGAACGCCCTGAACGGCAACGGGACCCCAACATGGAACAGAGCGCGT 300
Db 286 ACGCUUUGUCCAAAAGUCCCUUAAUUGGGAUCCGGGAUCCAAAUAAUAAUAAUAAUAAUAA 345
Qy 301 GAAGCTGTACAGGAGCTGAAGAGGAGATACCTTCCACGCGCGCGAGGAGATCAGGCT 360
Db 346 UAAACUGUAUAGGAAGCUAAAGAGGAGGAUAACAUAUCCUUGGGGCGAAAGAAUUAUCUACU 405
```

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Qy 361 GAGCTACAGCGCGCGCGCCCTGCGCAGCTGCTGATGGGCGCTGATCTACAAAGGATGGCGC 420
Db 406 CAGUUAUUCUGUGUGUGGACUUGCCAGUUGUAUUGGGCCUUAUACAACAGGAUGGGGC 465
Qy 421 CGTGACCAACGAGGTGGCCCTTTCGGCTGTGTGCGCCACCTGCGAGCAGATCGCCGACAG 480
Db 466 UGUGACCAUUAAGUGGCAUUGGCGUUGUUGGCAUCCUGUGAACAGAUUGUGUAGUC 525
Qy 481 CCAGCACCGCAGCCAGCAGCAGATGTGTGACCAACCAACCCCTGTGTGAGGCAACGAA 540
Db 526 CCAGCAUCGCGUCUUAUGGCAUUGGCAUUAUGGCAUUAUGGCAUUAUGGCAUUAUGGCA 585
Qy 541 CAGGATGTGCTGCGCAGCAGCACCGCCAAAGGCCATGGAGCAGATGCCCGCGCAGCAGGA 600
Db 586 CAGAAUGGUUUUAGCCAGCAGCUACAGCUAAGGCUAUGGAGCAAAUGGCUUGGAGUGA 645
Qy 601 GCAGGCGCGAGGCGCATGGAGGTGGCCAGCCAGGCGCAGGAGATGTGTGAGGCGCATGAG 660
Db 646 GCAAGCAGCAGAGCGCAUGAGGUGUUGUAGUCUAGGCUAAUUGGUGUAGGCGAGUGAG 705
Qy 661 GACCATCGGCACCAACCCAGCAGCAGCGCGCCCTTGAAGAACACCTGTGTGAGAACTAGT 720
Db 706 AACCAUUGGACUACUCCUAGCUCUAGGUGUGGCUUGAUAUUAUUAUUAUUAUUAUUA 765
Qy 721 GCAGGCTTACCAAGAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGAACCTAGT 775
Db 766 GCAGGCGCUAUCAGAAACGAAUUGGGGUGCAGAUAGCAACGCGUUAAGUGAAACUAGU 820

RESULT 6
US-10-729-830-1
; Sequence 1, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: Optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Influenza virus
; FEATURE:
; OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
US-10-729-830-1

Query Match 64.4%; Score 498.8; DB 8; Length 774;
Best Local Similarity 77.8%; Pred. No. 4.2e-109;
Matches 602; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

Qy 1 AGATCTAAAGATGAGCTGTGACCGAGGTGGAGACCTTACGTGTGAGCATCATCCCCAG 60
Db 1 AGATCTAAAGATGAGTCTTCTAACCGAGGTGCGAAACGTACGTTCTCTCTATCATCCCCGC 60
Qy 61 CGGCCCCCTGAAGCGCGAGATCGCCAGAGGCTGGAGAGCTGTGTGCGCGCGAAGAACAC 120
Db 61 AGGCCCCCTCAAGCGCGAGATCGCCAGAGAGCTGTGTGCGCGCGAAGAACAC 120
Qy 121 CGACCTGGAGTGTGTGATGGAGTGGCTGAAGACGAGGCGCCATCTGTAGCCCCCTGACCAA 180
Db 121 CGATCTTGAGGTCTTCATGGATGGCTTAAGACAAGACCAATCTGTCACTCTGACTTAA 180
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QY 1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTAGCTGCTGAGCATCATCCCGAG 60
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 16 ATATTGAAGATGAGTCTTTAAACCGAGGTGAAACGTACGTTCTCTCTATCATCCCGTC 75
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 CGGCCCTTGAAGCCGAGATCGCCAGAGGCTGGAGAGCTGTTCGCCGCGAAGAACAC 120
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76 AGGCCCTTAAAGCCGAGATCGCACAGACTTTGAAGATGTCTTTGAGGGGAAGAACAC 135
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CGACTCGAGGTGCTGATGGAGTGGCTGAAGACAGGCCCATCTGAGCCCCCTGACCAA 180
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAA 195
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GGGCATCTGGCTTCTGTTCACCTGACCGTCCAGAGCGCGGCTGACGCCG 240
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 196 GGGGATTTAGGATTTGTGTTTACCGCTCACCGTCCAGTGGAGGAGCTGCGCGTAG 255
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 CCGCTTCGTGCAGAACCCCTGAACGCGACCGGACCCCAACCAACATGACCAAGGCCGT 300
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 256 ACGCTTTGTCCAAATGCCCTTAATGGAAAGCGGGATCCAAATAAACATGACCAAGCAGT 315
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGCGCCCAAGGAGATCAGCCT 360
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 TAAACTGTATAGGAAGCTCAAGAGGAGATAACATTCCATGGGSCCAAAGAAATCTCACT 375
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 GAGCTACAGCGCCGCGCCCTGGCCAGCTGCAATGGGCTGATCTACAAAGGATGGCGC 420
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 CAGTTATTCTGCTGGTGCACTTGGCCAGTTGTATGGGCTTCATATACCAAGGATGGGGGC 435
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 CGTGACCAACGAGGTGGCTTGGGCTGGTGTGCGCACCTGCGAGCAGATGCGCGACAG 480
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 436 TGTGACCACTGAAGTGGCAATTTGGCTGGTATGTGCAACCTGTGAAACAGATGTCTGACTC 495
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 CCAGCACCGCAGCACAGGAGATGGTGACCAACCAACACCCCTGATCAGGCGACGAGAA 540
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 CCAGCATCGGTCTCATAGGCAAAATGGTGACAAACCAACCACTAATCAGACATGAGAA 555
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 541 CAGATGGTGTGGCCAGCACACCGCAAGGCCATGGAGCAGATGGCGGCGCAGCGGA 600
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 556 CAGAATGGTTTTAGCCAGCACTACAGCTTAAGGCTATGGAGCAAAATGGCTGGATCGAGTGA 615
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 GCAGCGCCGCGAGCCATGGAGGTGGCCAGCGAGGCGAGGATGGTGACGGCCATGAG 660
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 616 GCAAGCAGCAGAGGCCATGGAGGTGCTAGTCAGGCTAGGCAATGGTGCAAGCGATGAG 675
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 661 GACCATCGGCACCCACCGCAGCAGCGCGGCTGGAAGAACGACCTGTGGAGAACCT 720
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 676 AACCATGGGACTCATCTAGCTCCAGTGTGCTGTAAGAAATGATCTTCTTGAATAATT 735
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 721 GCAGGCTTACAGAAAGCGATGGGGTGCAGATGCGAGCGCTTCAAGTGAAC 771
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 736 GCAGGCTTATCAGAAACGAATGGGGTGCAGATGCAACGGTTCAAGTGATC 786
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

## RESULT 9

```
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065.133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18503
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
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; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1
```

```
Query Match 62.9%; Score 487.4; DB 6; Length 1023;
Best Local Similarity 76.9%; Pred. No. 2.2e-106;
Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;

QY 1 AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTAGCTGCTGAGCATCATCCCGAG 60
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15 ATATTTAAGATGAGTCTTCTGACCGAGGTGGAACGTACGTTCTCTCTATCGTACCATC 74
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 CGGCCCTTGAAGCCGAGATCGCCAGAGGCTGGAGGACGTGTTGCCGCGAAGAACAC 120
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75 AGGCCCTTCAAAGCCGAGATCGCGCAGACATTTGAAGATGTCTTTGAGGGGAAGAACAC 134
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACAGGCCCATCTGAGCCCCCTGACCAA 180
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 CGATCTTGAGGCACTCATGGAATGGCTTAAAGACAAGACCAATCTGTCACTCTGACTAA 194
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GGGCATCTGGGCTTCTGTTCACCTGACCGTCCAGAGCGCGGCTGACGCCCG 240
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 195 AGGATTTTAGGATTCGTATTTCACGCTCACCGTCCAGTGGAGGAGCTGCGACGCTAG 254
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 CCGCTTCGTGCAGAACCCCTGAAACGGCAACCGGACCCCAACCAACATGACCAAGGCCGT 300
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 255 ACGCTTTGTCCAAATGCCCTTAGTGGAACCGGAGATCCAACCAACATGCGAGAGCAGT 314
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACCTTCCACGCGCCCAAGGAGATCAGCCT 360
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 AAAACTGTACAGGAAGCTTAAAGAGAAATAAATTCATCCATGGGCAAAAGAGGTGGCACT 374
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 GAGCTACAGCGCGCGCCCTGGCCAGCTGCATGGGCTGATCTACAAAGGATGGCGGC 420
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 CAGCTATTCACCTGGTGCACTAGCCAGCTGCATGGGACTCATATACAAAGAAATGGGAAC 434
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 CGTGACCAACCGAGGTGGCCCTTGGGCTGTGTGGCCACCTGCGAGCAGATCGCGCAGAC 480
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 435 TGTGACAAACGGAAGTGGCAATTTGGCCTGGTATGGCCACATGTGAAACAGATCGCTGATTC 494
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 CCAGCACCGCAGCCACAGGCGAGATGGTGACCAACCAACCCCTGATCAGGCGACGAGAA 540
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 495 CCAGCATCGATCTCAGAGGAGATGGTGACAAACCAACCCATTAATCAGACATGAANA 554
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 541 CAGGATGGTGTGGCCAGCACACCGCCAAAGGCCATGGAGCAGATGGCGGCGCAGACGGA 600
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 555 CAGAAATGGTATTAGCCAGTACCACGGCTTAAGCCATGGAGCAGATGCGAGGTGAGTGA 614
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 GCAGGCGCGCAGGCCATGAGAGTGGCCAGCGCCAGGCGCAGGAGATGGTGAGGCGCATGAG 660
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 615 GCAGGCGCAGAGGCCCATGGAGGTGCTAGTAGGGCTAGGCGAGATGGTRCAGGCAATGAG 674
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 661 GACCATCGGCACCCACCGCAGCAGCGCGGCTGGAAGAACGACCTGTGGAGAACCT 720
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 675 AACCATGGGACCCACCCCTAGCTCCAGTGGCGGTTTGAAGATGATCTTCTTGAATAATT 734
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 721 GCAGGCTTACAGAAAGCGCATGGGCGTGCAGATGCGAGCGCTTCAAGTGAAC 771
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 735 GCAGGCTTACAGAAACGGATGGGAGTGCAAAATSCAGCGATTCAGTGATC 785
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

## RESULT 10

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US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Publication No. US20040022809A1
```



GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-CI-PUS-1  
; CURRENT APPLICATION NUMBER: US/10/434,811A  
; CURRENT FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION:  
; NAME/KEY: misc feature  
; LOCATION: (663)..(663)  
; OTHER INFORMATION: At nucleotide 663, r = a or g  
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val  
; US-10-434-811A-1

Query Match 62.9%; Score 487.4; DB 7; Length 1023;  
Best Local Similarity 76.9%; Pred. No. 2.2e-106;  
Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;  
  
Qy 1 AGATCTAAAGATGAGCTGTGACCGAGGTGGAGACCTACTGTGTGAGCATCATCCCCAG 60  
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGCAAAACGTACCTTCTCTATCGTACCATC 74  
  
Qy 61 CGGCCCCCTGAAGCCGAGATCGCCGAGAGCTGGAGACCTGTTCCGCGCAGAACAC 120  
Db 75 AGGCCCCCTCAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTGAGGGAAGAACAC 134  
  
Qy 121 CGACTGTGAGTGTGTGATGAGTGGCTGAAGACGAGGCCATCTGTGAGCCCCCTGACCAA 180  
Db 135 CGATCTTGAGGCACTCATGAGTGGCTAAAGACAGACCATCTGTCACTCTGACTAA 194  
  
Qy 181 GGGCATCTGGGCTTGTGTTTCACTGACCGTCCGAGCGAGCGCGCTGACAGCGCG 240  
Db 195 AGGGATTTTAGGATTTGATTTACGCTCACCGTGCAGTGGAGGAGTGCAGCGTAG 254  
  
Qy 241 CGGCTTCTGAGACGCGCTTGAACGGCAACGGCGACCCCAACATGGAACAGGCGCT 300  
Db 255 ACGCTTTGTCCAAATGCGCTTAGTGGAAACGGAGATCCAAACCAACATGGAACAGCAGT 314  
  
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACTTCCAGCGCGCAGAGAGATCAGGCT 360  
Db 315 AAAAGCTGTACAGGAAGCTTAAAGAGAAATTAACATTCATCGGGGCAAGAGGTTGCACT 374  
  
Qy 361 GAGCTTACAGCGCGCGCTTGGCGAGCTGTGATGGGCTGATCTACAAAGAGTGGGCGC 420  
Db 375 CAGCTATTCCACTGGTGCATAGCCAGCTGCATGGGACTCATATACACAGAAATGGGAAC 434  
  
Qy 421 CGTGACACCGAGGTGGGCTTGGGCTGTGTGGCCACCTGCGAGCGAGATCGCGACAG 480  
Db 435 TGTGACAAACCGAAGTGGGCTTGGGCTGTGTGGCCACATGTGAACAGATCGGTGATTC 494  
  
Qy 481 CCAGCACCGCAGCAGGAGATGGTGAACCAACCAACCCCTGATCAGGCGACGAGAA 540  
Db 495 CGAGCATCGATCTCACAGGAGATGGTGAACCAACCAACCCATTAATCAGACATGAATA 554  
  
Qy 541 CAGGATGTGTGGCGCAGCACCAACCGCAAGGCCATGAGGAGATGGCGCAGCAGCGA 600  
Db 555 CAGAATGTATTAGCCAGTACCACGGCTTAAGGCCATGAGGAGATGGCAGGCTCGAGTGA 614

Qy 601 GCAGGCGCGCAGGCGCATGAGGTGGCCAGCCAGGCGCAGAGTGTGAGGCGCATGAG 660  
Db 615 GCAGGCGCAGAGGCGCATGAGGTGGCTAGTAGGCTAGGCGATGTRCAGGCAATGAG 674  
  
Qy 661 GACATCGGCAACCCAGAGCGCGCGCTGGAAGAACGACCTGCTGGAGAACCT 720  
Db 675 AACCATTTGGGACCCACCTAGCTCCAGTGCCTGTTGAAAGATGATCTCCTTGAATAATTT 734  
  
Qy 721 GCAGGCGCTACCAAGAGCGCATGCGCGTGCAGATGCGAGCGCTTCAAGTGAAC 771  
Db 735 GCAGGCGCTACCAAGAACCGATGGAGTGCAGATGCGAGCGATTCAGTGAATC 785  
  
RESULT 11  
US-10-734-373-1  
; Sequence 1, Application US/10734373  
; Publication No. US20040137015A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/734,373  
; CURRENT FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION:  
; NAME/KEY: misc feature  
; LOCATION: (673)..(673)  
; OTHER INFORMATION: At nucleotide 673, r = a or g  
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val  
; US-10-734-373-1

Query Match 62.9%; Score 487.4; DB 7; Length 1023;  
Best Local Similarity 76.9%; Pred. No. 2.2e-106;  
Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;  
  
Qy 1 AGATCTAAAGATGAGCTGTGACCGAGGTGGAGACCTACTGTGTGAGCATCATCCCCAG 60  
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGCAAAACGTACCTTCTCTATCGTACCATC 74  
  
Qy 61 CGGCCCCCTGAAGCCGAGATCGCCGAGAGCTGGAGACCTGTTCCGCGCAGAACAC 120  
Db 75 AGGCCCCCTCAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTGAGGGAAGAACAC 134  
  
Qy 121 CGACTGTGAGTGTGTGATGAGTGGCTGAAGACGAGGCCATCTGTGAGCCCCCTGACCAA 180  
Db 135 CGATCTTGAGGCACTCATGGAATGGCTTAAAGACAGACCAATCTGTCACTCTGACTAA 194  
  
Qy 181 GGGCATCTGGGCTTGTGTTTCACTGACCGTCCGAGCGAGCGCGCTGACAGCGCG 240  
Db 195 AGGGATTTTAGGATTTGATTTACGCTCACCGTGCAGTGGAGGAGTGCAGCGTAG 254  
  
Qy 241 CGGCTTCTGAGACGCGCTTGAACGGCAACGGCGACCCCAACATGGAACAGGCGCT 300  
Db 255 ACGCTTTGTCCAAATGCGCTTAGTGGAAACGGAGATCCAAACCAACATGGAACAGCAGT 314  
  
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACTTCCAGCGCGCAGAGATGAGGCT 360  
Db 315 AAAAGCTGTACAGGAAGCTTAAAGAGAAATTAACATTCATCGGGGCAAGAGGTTGCACT 374







```

; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; US-10-434-811A-4

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| Query Match           | 62.5% | Score 484.6   | DB 7           | Length 1023 |
|-----------------------|-------|---|----------------|-------------|
| Best Local Similarity | 76.8% | Pred. No.1e-105   |                |             |
| Matches               | 592   | Conservative 0  | Mismatches 179 | Indels 0    |
| Qy                    | 1     | AGATCTAAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG      | 60             |             |
| Db                    | 15    | ATATTTAAAGATGAGTCTTCTGACCGAGGTGGAAACGTACGTTCTCTCTATCTTACCATC      | 74             |             |
| Qy                    | 61    | CGGCCCTCTGAAGCCGAGATCGCCACGAGGCTGGAGACGTGTTCCGCGGCAAGAACAC        | 120            |             |
| Db                    | 75    | AGGCCCTCTAAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTGCAGGAGNAGACAC        | 134            |             |
| Qy                    | 121   | CGACTTGGAGGTGCTGATFGAGTGGCTGAAGACAGGCCCATCTCTAGCCCCCTGACCAA       | 180            |             |
| Db                    | 135   | CGATCTTTGAGGCACTCATGGAATGGCTAAAGACAAGCAATCTGTCAACCTCTGACTAA       | 194            |             |
| Qy                    | 181   | GGGCATCTGGGCTTTGGTTTCAACCTGACCGTCCGACGAGCGCGCCTGACAGCGCG          | 240            |             |
| Db                    | 195   | AGGGAATTTTAGGATTCGTTATTTCAACGCTCACCGTCCGAGTGGAGGAGACTGACGCGT      | 254            |             |
| Qy                    | 241   | CCGCTTCTGTGACGAACGCCCTGAAACGGCAACGGCGACCCCAACCAACATGGCAAGGCCGT    | 300            |             |
| Db                    | 255   | ACGCTTTTCCAAATGCCCTTAGTGGNAAACGGAGATCCAAACAACATGGACAGAGCAGT       | 314            |             |
| Qy                    | 301   | GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCAAGGAGATCAGGCT       | 360            |             |
| Db                    | 315   | AAAACTGTACAGGAAGCTTAAAGAGAGAAATTAACATTCCATGGGGCAAAAGAGGTGGCACT    | 374            |             |
| Qy                    | 361   | GAGCTACAGCGCGCGCCCTGGCCAGCTGCATGGCTGATCTACAAACAGGATGGGCGC         | 420            |             |
| Db                    | 375   | CAGCTATTCCACTGGTGACCTAGCCAGCTGCATGGGACTCATATACAAACAATGGGAAC       | 434            |             |
| Qy                    | 421   | CGTGACCAACCGAGGTGGGCTTTGGGCTGGGCCACCTTCGACGACAGATCGCCGACAG        | 480            |             |
| Db                    | 435   | TGTGACAAACGAATGGCAATTTGGCTTGGTATGGCCACATGTGACAGATCGCTGATTC        | 494            |             |
| Qy                    | 481   | CCAGCACCGCACCAAGGACAGATGGTGAACCAACCAACCCCTGTATCAGGCAAGAGAA        | 540            |             |
| Db                    | 495   | CCAGCATCGATCTCACAGGACAGATGGTGACAAATTAACCAACCAATTAATCAGACATGAAA    | 554            |             |
| Qy                    | 541   | CAGATGGTGTGGCCACGACCAACCGCCATGGAGGCAATGGAGCAGATGGCCGACAGCGA       | 600            |             |
| Db                    | 555   | CAGAAATGGTATTTAGCCAGTACCAACGCTTAAGCCATGAGCAGATGGCAGGGTTCAGTGA     | 614            |             |
| Qy                    | 601   | GCAGGCGCCGAGGCCATGAGAGGTGGCCACGACGACAGGACAGATGGTGCAGGCCATGAG      | 660            |             |
| Db                    | 615   | GCAGGCACGACAGGCCATGGAGGTTGCTAGTAAAGGCTAGGACAGATGGTACAGGCNAATG     | 674            |             |
| Qy                    | 661   | GACCATCGGCAACCAACCCACGACGAGCGCGGCTGAAGAACCGACTGTCTGGAGAACCT       | 720            |             |
| Db                    | 675   | AACCAATTTGGGACCAACCCCTAGCTCAAGTCCGCGGTTGAAGAGATGATCTCTTTGAAAAATTT | 734            |             |



```
Qy 191 GGCTTCGTGTTACCCCTGACCGTGCACGAGCGCGGCTGCGAGCGCGCGCTTCGTG 250
Db 181 GGCTTCGTGTTACCCCTGACCGTGCACGAGAGAGGGGCTGCGAGAGAGAGGTTCCGTG 240
Qy 251 CAGAAAGCCCTTGAAACGGCAACGGCGACCCCAACAACATGGACAAAGGCGCTGAAAGCTGTAC 310
Db 241 CAGAAAGCCCTTGAAACGGCAACGGCGACCCCAACAACATGGACAAAGGCGCTGAAAGCTGTAC 300
Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCCAAGGAGATCAAGCTGAGCTACAGC 370
Db 301 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCCAAGGAGATCAAGCTGAGCTACAGC 360
Qy 371 GCCGGCGCCCTGGCCAGCTGATGGGCTGTATCTACAACAGGATGGGGCGCGCTGACCAAC 430
Db 361 GCCGGCGCCCTGGCCAGCTGATGGGCTGTATCTACAACAGGATGGGGCGCGCTGACCAAC 420
Qy 431 GAGGTGGCTTTCGGGCTTGGTGGCGCACCTGCGAGCAGATCGCGGACAGCCAGCACCGC 490
Db 421 GAGGTGGCTTTCGGGCTTGGTGGCGCACCTGCGAGCAGATCGCGGACAGCCAGCACAGG 480
Qy 491 AGCCACAGGCGAGATGGTGACCAACCAACCCCTGTATCAGGCAACGAGAAACAGGATGGTG 550
Db 481 AGCCACAGGCGAGATGGTGACCAACCAACCCCTGTATCAGGCAACGAGAAACAGGATGGTG 540
Qy 551 CTGCGCAGCACCAACCGCAAGGCCATGGAGCAGATGGCGGCGCAGCAGGAGCGCGCC 610
Db 541 CTGCGCAGCACCAACCGCAAGGCCATGGAGCAGATGGCGGCGCAGCAGGAGCGCGCC 600
Qy 611 GAGGCCATGAGAGTGGCGAGCCAGCCAGGCGAGATGGTGAGGCGCATGAGGACCATCGGC 670
Db 601 GAGGCCATGAGAGTGGCGAGCCAGGCGAGGCGAGATGGTGAGGCGCATGAGGACCATCGGC 660
Qy 671 ACCCAACCCAGCAGCAGCGCGGCTGAAAGAACGACCTGTCTGGAGAACCTGCGAGGCTTAC 730
Db 661 ACCCAACCCAGCAGCAGCGCGGCTGAAAGAACGACCTGTCTGGAGAACCTGCGAGGCTTAC 720
Qy 731 CAGAAGCGCATGGGCGTGCAGATGACGGCTTCAAG 766
Db 721 CAGAAGAGGATGGGCGTGCAGATGACGAGGTTCAAG 756
```

## RESULT 2

```
US-11-131-479-59
; Sequence 59, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for the M2M1 Fusion from VR4755
US-11-131-479-59
Query Match 89.4%; Score 692.8; DB 12; Length 1050;
Best Local Similarity 93.9%; Pred. No. 9.1e-141;
Matches 721; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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Qy 2 GATCTAAGATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGC 61

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Db 283 GAGCTGGAGATGTCCTGCTGACAGAAAGTGGAACATACGTGCTGAGCATCTGCCCCAGC 342
Qy 62 GGCCCCCTGAAGCCGAGATCGCCAGAGGCTGGAGACGTGTTGCGCCGCGCAAGAACACC 121
Db 343 GGCCCCCTGAAGCCGAGATCGCCAGAGACTGGAGACGTGTTGCGCCGCGCAAGAACACC 402
Qy 122 GAGCTGGAGGTGCTGATGGAGTGGCTGAAAGACAGAGCCCATCTGTAGCCGCCCTGACCAAG 181
Db 403 GAGCTGGAGGCCCTGATGGAGTGGCTGAAAGACAGAGCCCATCTGTAGCCGCCCTGACCAAG 462
Qy 182 GGCATCTCGGCTTCGTGTTACCTGACCGTGCAGCGGCGGCGGCTGCGAGCGCGC 241
Db 463 GGCATCTCGGCTTCGTGTTACCTGACCGTGCAGCGGCGGCGGCTGCGAGAGAGA 522
Qy 242 CGCTTCGTGAGAACCGCCCTGAAACGGCAACGGCGACCCCAACAACTGGAAGAGCCCGTG 301
Db 523 AGATTGCTGAGAACCGCCCTGAAACGGCAACGGCGACCCCAACAACTGGAAGAGCCCGTG 582
Qy 302 AGCTGTACAGGAAGCTGAGAGGGAGATCACCTTCCACGGCGCCAGGAGATCAGCCTG 361
Db 583 AGCTGTACAGGAAGCTGAGAGGGAGATCACCTTCCACGGCGCCAGGAGATCAGCCTG 642
Qy 362 AGCTACAGCGCCGCGGCTTGGCCAGCTGCATGGGCTGTATCTACAACAGATGGGCGCC 421
Db 643 AGCTACAGCGCCGCGGCTTGGCCAGCTGCATGGGCTGTATCTACAACAGATGGGCGCC 702
Qy 422 GTACACCAACGAGTGGCTTTCGGCTTGGTGGCGCACCTGCGAGCAGATGCGCGCAAGC 481
Db 703 GTACACCAACGAGTGGCTTTCGGCTTGGTGGCGCACCTGCGAGCAGATGCGCGCAAGC 762
Qy 482 CAGCACCGCAGCCACAGGCGAGATGGTGACCAACCAACCAACCCCTGTATCAGGCGAGAAC 541
Db 763 CAGCACAGAAAGCCACAGACAGATGGTGGCGCACCAACCAACCCCTGTATCAGACAGAAC 822
Qy 542 AGGATGCTGTGCGCAGCACACCGCCAGGCGCATGGAGCAGATGGCGCGCAGCAGCGAG 601
Db 823 AGAATGCTGTGCGCAGCACACCGCCAGGCGCATGGAGCAGATGGCGCGCAGCAGCGAG 882
Qy 602 CAGGCGCGCCAGGCGCATGGAGTGGCGAGCCAGCGGCGCAGGCGAGATGTTGCGAGGCGCATGAGG 661
Db 883 CAGGCGCGCCAGGCGCATGGAGATCGCCAGCGCAGGCGCAGACAGATGGTGCAGGCGCATGAGA 942
Qy 662 ACATCGGCGACCCACCCAGCAGCGCGCGGCTGAAAGAACGACCTGTGAGAGAACCTG 721
Db 943 GCCATCGGCGACCCACCCAGCAGCGCGCGGCTGAAAGAACGACCTGTGAGAGAACCTG 1002
Qy 722 CAGGCGCTTACCAGAAAGCGCATGGGCGTGCAGATGCGCGCTTCAAGTGA 769
Db 1003 CAGACCTACCAGAAAGAGATGGGCGTGCAGATGCGAGAGATTCAAGTGA 1050
```

## RESULT 3

```
US-11-131-479-69
; Sequence 69, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
; LENGTH: 759
```

```

; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for M1 Gene from VR4760
US-11-131-479-69

Query Match      88.9%; Score 688.6; DB 12; Length 759;
Best Local Similarity 94.2%; Pred. No. 7.5e-140;
Matches 715; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 11 ATGAGCTGCTGACCGAGGTGGAGACCTACGTCTGAGCATATCCCGAGGGCCCCCTG 70
Db 1 ATGTCCTCTGCTGACAGAGTGGAAACATACGTCTGAGCATGTCGCCAGCGCCCCCTG 60

Qy 71 AAGGCCGAGATCGCCAGAGCTGAGGACGTGTTCCGCCGGAAGAACACCGACCTGAG 130
Db 61 AAGGCCGAGATCGCCAGAGCTGAGGACGTGTTCCGCCGGAAGAACACCGACCTGAG 120

Qy 131 GTGCTGATGGAGTGGCTGAAGACAGGCGCCATCTCTGAGCCCTCTGACCAAGGGATCTG 190
Db 121 GCCCTGATGGAGTGGCTGAAGACAGGCGCCATCTCTGAGCCCTCTGACCAAGGGATCTG 180

Qy 191 GGCTTCGTGTTCACTGACCGTGCAGAGCGCGCCCTGAGCGCGCCGCTTCTG 250
Db 181 GGCTTCGTGTTCACTGACCGTGCAGAGCGCGCCCTGAGCGCGCCGCTTCTG 240

Qy 251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACACATGGACAAAGGCCGTGAAGCTGTAC 310
Db 241 CAGAACGCCCTGAACGGCAACGGCGACCCCAACACATGGACAAAGGCCGTGAAGCTGTAC 300

Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAGAGAGATCAGCTGAGCTACAGC 370
Db 301 CGGAAGCTGAAGAGAGATCACCTTCCACGGCGCCAGAGAGATCAGCTGAGCTACAGC 360

Qy 371 GCCGGCGCTTGGCGAGCTGATGGGCTGTATCTACAAAGAGTGGGCGCGCTGACCAAC 430
Db 361 GCCGGCGCTTGGCGAGCTGATGGGCTGTATCTACAAAGAGTGGGCGCGCTGACCAAC 420

Qy 431 GAGTGGCTTGGCGCTTGGTGGCCACCTGCGCAGCAGATCGCGCAGCAGCAGCAGCGC 490
Db 421 GAGTGGCTTGGCGCTTGGTGGCCACCTGCGCAGCAGATCGCGCAGCAGCAGCAGCGC 480

Qy 491 AGCCACAGCAGATGGTGACCAACACCCCTGTATCAGGCACGAGAACAGGATGGTG 550
Db 481 AGCCACAGCAGATGGTGACCAACACCCCTGTATCAGGCACGAGAACAGGATGGTG 540

Qy 551 CTGGCCAGCAACACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCGCC 610
Db 541 CTGGCCAGCAACACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCGCC 600

Qy 611 GAGGCCATGGAGTGGCGCAGCGCCAGCGCAGATGGTGAGGCCATGAGGACCATCGGC 670
Db 601 GAGGCCATGGAGTGGCGCAGCGCCAGCGCAGATGGTGAGGCCATGAGGACCATCGGC 660

Qy 671 ACCCAACCCAGCAGCAGCGCGCTGAAAGAACGACCTGTGAGAGAACCTGACGCGCTAC 730
Db 661 ACCCAACCCAGCAGCAGCGCGCTGAAAGAACGACCTGTGAGAGAACCTGACGAGCTAC 720

Qy 731 CAGAAGCGCATGGGCGTGCAGATGACGCGCTTCAAGTGA 769
Db 721 CAGAAGAGAAATGGGCGTGCAGATGACAGATTTCAAGTGA 759
```

RESULT 4

```

US-11-131-479-61
; Sequence 61, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
```

```

; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Codon Optimized Segment 7 from VR4763
US-11-131-479-61
```

```

Query Match      86.2%; Score 668.2; DB 12; Length 982;
Best Local Similarity 92.4%; Pred. No. 1.9e-135;
Matches 703; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 11 ATGAGCTGCTGACCGAGGTGGAGACCTACGTCTGAGCATATCCCGAGGGCCCCCTG 70
Db 1 ATGAGCTGCTGACCGAGGTGGAACGTATGTTCTCTATCTGTCGCCAGCGCCCCCTG 60

Qy 71 AAGGCCGAGATCGCCAGAGCTGGAGAGCTGTTCCGCCGGAAGAACACCGACCTGAG 130
Db 61 AAGGCCGAGATCGCCAGAGCTGGAGAGCTGTTCCGCCGGAAGAACACCGACCTGAG 120

Qy 131 GTGCTGATGGAGTGGCTGAAGACAGGCGCCATCTCTGAGCCCTCTGACCAAGGGATCTG 190
Db 121 GCCCTGATGGAGTGGCTGAAGACAGGCGCCATCTCTGAGCCCTCTGACCAAGGGATCTG 180

Qy 191 GGCTTCGTGTTCACTGACCGTGCAGAGCGCGCCCTGAGCGCGCCGCTTCTG 250
Db 181 GGCTTCGTGTTCACTGACCGTGCAGAGCGCGCCCTGAGCGCGCCGCTTCTG 240

Qy 251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACACATGGACAAAGGCCGTGAAGCTGTAC 310
Db 241 CAGAACGCCCTGAACGGCAACGGCGACCCCAACACATGGACAAAGGCCGTGAAGCTGTAC 300

Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAGAGAGATCAGCTGAGCTACAGC 370
Db 301 AGAAGCTGAAGAGAGAGATCACCTTCCACGGCGCCAGAGAGATCAGCTGAGCTACAGC 360

Qy 371 GCCGGCGCTTGGCGAGCTGATGGGCTGTATCTACAAAGAGTGGGCGCGCTGACCAAC 430
Db 361 GCCGGCGCTTGGCGAGCTGATGGGCTGTATCTACAAAGAGTGGGCGCGCTGACCAAC 420

Qy 431 GAGTGGCTTGGCGCTTGGTGGCCACCTGCGCAGCAGATCGCGCAGCAGCAGCAGCGC 490
Db 421 GAGTGGCTTGGCGCTTGGTGGCCACCTGCGCAGCAGATCGCGCAGCAGCAGCAGCGC 480

Qy 491 AGCCACAGCAGATGGTGACCAACACCCCTGTATCAGGCACGAGAACAGGATGGTG 550
Db 481 AGCCACAGCAGATGGTGACCAACACCCCTGTATCAGGCACGAGAACAGGATGGTG 540

Qy 551 CTGGCCAGCAACACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCGCC 610
Db 541 CTGGCCAGCAACACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCGCC 600

Qy 611 GAGGCCATGGAGTGGCGCAGCGCCAGCGCAGATGGTGAGGCCATGAGGACCATCGGC 670
Db 601 GAGGCCATGGAGTGGCGCAGCGCCAGCGCAGATGGTGAGGCCATGAGGACCATCGGC 660

Qy 671 ACCCAACCCAGCAGCAGCGCGCTGAAAGAACGACCTGTGAGAGAACCTGACGCGCTAC 730
Db 661 ACCCAACCCAGCAGCAGCGCGCTGAAAGAACGATCTTCTTGAAGATTTTTCAGACCTAT 720

Qy 731 CAGAAGCGCATGGGCGTGCAGATGACGCGCTTCAAGTGAAC 771
Db 721 CAGAAGCAATGGGCGTGCAGATGACACGATTCAGTGACC 761
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```
RESULT 5
US-11-131-479-79
; Sequence 79, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 79
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Optimized M1 Coding Region
US-11-131-479-79

Query Match      86.2%; Score 667.8; DB 12; Length 759;
Best Local Similarity 92.5%; Pred. No. 2.3e-135; Indels 0; Gaps 0;
Matches 702; Conservative 0; Mismatches 57;

Qy 11 ATGAGCTGTGCTGACCGAGGTGGAGACCTACGTCTGTGAGCATCATCCCCAGCGGCCCTG 70
Db 1 ATGAGCTGTGCTGACCGAGGTGGAGACCTATGTTCTCTATCGTCCAGCGGCCCTG 60

Qy 71 AAGCCGAGATCGCCGAGAGCTGGAGACGTGTTGCGCGCAAGAACACCGACCTGGAG 130
Db 61 AAGCCGAGATCGCCGAGAGCTGGAGACGTGTTGCGCGCAAGAACACCGACCTGGAG 120

Qy 131 GTGCTGATGGAGTGGCTGAACAGCAGGCGCCATCTGTAGGCCCTGACCAAGGGATCCTG 190
Db 121 GCCCTGATGGAGTGGCTGAACAGCAGCACCCTCTGTAGGCCCTGACCAAGGGATCCTG 180

Qy 191 GGCTTCGTGTTTACCTTACCTGACCGTGCACGAGAGCGCGCTGACGCGCGCGCTTCGTG 250
Db 181 GGCTTCGTGTTTACCTTACCTGACCGTGCACGAGAGCGCGCTGACGCGCGCGCTTCGTG 240

Qy 251 CAGAACCGCTGAACGGCAACGGCGACCCCAACCAACATGGACAGGCGCGTGAAGCTGTAC 310
Db 241 CAGAACCGCTGAACGGCAACGGCGACCCCAACCAACATGGACAGGCGCGTGAAGCTGTAC 300

Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAAGAGATCAAGCTGAGTACAGC 370
Db 301 AGAAGCTGAAGAGGGAGATCACATTTCAATGGCGCCAAAGAGATATCGCTGAGTACAGT 360

Qy 371 GCAGCGCCCTTGGCCAGCTGCGGCTCATCTAGAACAGGATGGCGCGCGTACACACC 430
Db 361 GCAGCGCCCTTGGCCAGCTGCGGCTCATCTAGAACAGGATGGCGCGCGTACACACC 420

Qy 431 GAGTGGCTTGGCGCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCAGCAGCCGC 490
Db 421 GAGTGGCTTGGCGCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCAGCAGCCGC 480

Qy 491 AGCCACAGCAGATGGTGCACCAACCAACCCCTGATCAGCGACGAGAACAGGATGGT 550
Db 481 AGCCACAGCAGATGGTGGCCACCAACCCCTGATCAGACACAGAACAGATGGT 540

Qy 551 CTGGCCAGCACACCGCCAAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCC 610
Db 541 CTGGCCAGCACACCGCCAAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCC 600

Qy 611 GAGGCCATGGAGTGGCGCAGCCAGGCCAGGCAGATGGTGTGAGGCCATGAGGACCATCGGC 670
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Db 601 GAGGCCATGGAGTGGCGCAGCCAGCCAGACACATGGTGCAGGCCATGAGGACCATCGGC 660
Qy 671 ACCCACCAGCAGCAGCGCGCTGAAGAACAGCCTGCTGGAGAACCTGCGAGGCTAC 730
Db 661 ACCCACCAGCAGCAGCGCGCTGAAGAGATGATCTTCTTGAATAATTTGCAGACCTAT 720
Qy 731 CAGAAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGA 769
Db 721 CAGAAACGAATGGGGTGCAGATGCAACGATTCAAGTGA 759

RESULT 6
US-11-131-479-28
; Sequence 28, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 28
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-28

Query Match      77.1%; Score 597.6; DB 12; Length 756;
Best Local Similarity 86.9%; Pred. No. 3.3e-120; Indels 0; Gaps 0;
Matches 657; Conservative 0; Mismatches 99;

Qy 11 ATGAGCTGTGCTGACCGAGGTGGAGACCTACGTCTGTGAGCATCATCCCCAGCGGCCCTG 70
Db 1 ATGAGCTGTGCTGACCGAGGTGGAGACCTATGTTCTCTATCGTCCATCATTCCTCAGCGGCCCTG 60

Qy 71 AAGCCGAGATCGCCGAGAGCTGGAGACGTGTTGCGCGCAAGAACACCGACCTGGAG 130
Db 61 AAGCCGAGATCGCCGAGAGCTGGAGACGTGTTGCGCGCAAGAACACCGACCTGGAG 120

Qy 131 GTGCTGATGGAGTGGCTGAAGACAGCGCCCATCTGTAGGCCCTGACCAAGGGATCCTG 190
Db 121 GTGCTGATGGAGTGGCTGAAGACTCGGCCCATCTGTCTCCCTGACCAAGGGATCCTG 180

Qy 191 GGCTTCGTGTTTACCTTACCTGACCGTGCACGAGGCGCGCTGACGCGCGCGCTTCGTG 250
Db 181 GGCTTCGTGTTTACCTTACCTGACCGTGCACGAGGCGCGCTGACGCGCGCGCTTCGTG 240

Qy 251 CAGAACCGCTGAACGGCAACGGCGACCCCAACCAACATGGACAGGCGCGTGAAGCTGTAC 310
Db 241 CAGAACCGCTGAACGGCAACGGCGACCCCAACCAACATGGATGAAGCGCTGAAGCTGTAT 300

Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAAGAGATCAAGCTGAGTACAGC 370
Db 301 AGAAGCTGAAGAGGGAGATCACATTTCAATGGCGCCAAAGAGATATCGCTGAGTACAGT 360

Qy 371 GCAGCGCCCTTGGCCAGCTGCGGCTCATCTAGAACAGGATGGCGCGCGTACACACC 430
Db 361 GCAGCGCCCTTGGCCAGCTTTCATATGAGAACAGATGGCGCGCGCTTACTACA 420

Qy 431 GAGTGGCTTGGCGCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCAGCAGCCGC 490
```



Db 421 GAGGTAGCCTTTGGCCTGCTGCGCCACTTTCGAGCAGATCGCGCATCTCAGCATAGA 480  
QY 491 AGCCACAGCAGATGGTCACACCAACCAACCCCTGATCAGCAGCAGCAAGAGATGGTG 550  
Db 481 TCTCAGACAGATGGTGACGACTACAAACCCCTGATACGGCAGCAGAAAGATGGTG 540  
QY 551 CTGGCCAGCACACCGCCCAAGGCCATGAGCAGCAGATGGCGGCGAGCAGCAGCGCCGCC 610  
Db 541 CTGGCCTCTACTACCGCCCAAGGCCATGAGCAGCAGATGGCGGCGAGCAGTGGAGCGCGCC 600  
QY 611 GAGGCCATGAGAGTGGCCAGCCAGCCAGCAGCAGATGGTGAGGCCATGAGCAGCAGTGGC 670  
Db 601 GAGGCCATGAGAGTGGCCAGCCAGCCAGCAGCAGATGGTGAGGCCATGAGCAGCAGTGGC 660  
QY 671 ACCACCCAGCAGCAGCGCGGCTGAAGAACGACCTGTGAGAACCTTCAGSCCTAC 730  
Db 661 ACTCACCCCTTCAGCTTCGCGGCTGAAGAACGACCTGTGAGAACCTTCAGSCCTAT 720  
QY 731 CAGAAGCGCATGGCGCTGCAGATGACGCGCTTTCAAG 766  
Db 721 CAGAAGAGATGGCGGTACAGATGACGAGGTTCAAG 756

## RESULT 7

US-11-131-479-26  
; Sequence 26, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131.479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 26  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein  
US-11-131-479-26

Query Match 63.4%; Score 491; DB 12; Length 756;  
Best Local Similarity 78.1%; Pred. No. 3.4e-97;  
Matches 590; Conservative 0; Mismatches 165; Indels 0; Gaps 0;  
QY 11 ATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATATCCCGAGCGGCCCTG 70  
Db 1 ATGAGCTTGCTAACAGAGTGGAAACCTATGTCTCAGTATCATCTCTAGCGGCCCTTA 60  
QY 71 AAGGCCAGATCGCCAGAGCTGGAGGACGTGTTCGCCGCAAGAACACCGACTGGAG 130  
Db 61 AAAGCCGAATCGCTCAGCGCTCGAGGATGTTTTTTCGCCGCAAGAACACCGACTGGAG 120  
QY 131 GTGCTGATGGATGGCTGAAGACCAAGGCCCATCTCTGAGCCCCCTGACCAAGGGATCCTG 190  
Db 121 GTATTGATGGATGGCTGAAGAACCGGACCTTATCTGAGCCCCCTGACTAAGGGGAATCTC 180  
QY 191 GCCTTCGTGTTTACCTCAGCGTCCAGCGAGCGCGCTGACGCGCGCGCTTCGTG 250  
Db 181 GCCTTCGTTTTTACATTGACCGTGCCTTCAGAGAGGGGTCTCCAAAGAGGCGCTTCGTG 240  
QY 251 CAGAACCGCTTGAACCGGCAACCGGACCCCAACACATGAGCAAGGCGGTGAAGCTGTAC 310  
Db 241 CAGAACCGCTTGAACCGGCAACCGGACCCCAACATATATGATATGAGGCAAGTGAACCTGTAT 300

QY 311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGGCCCAAGAGATCAGCTTGAGCTACAGC 370  
Db 301 CGCAATTAAGCGGGAGATAACCTTCCATGGAGCCAAAGGAGATCTCCCTGCTTACTCT 360  
QY 371 GCCGGCCCTTGGCCAGCTGCATGGGCTGATCTACCAAGAGATGGGCGCGCTGACCAACC 430  
Db 361 GCAGGTGCTCTCGCGCTGCTGTATGGGACTTATCTACAAACCGAATGGGCGCGCTCAACA 420  
QY 431 GAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAGATCGCGGACAGCAGCAGCCG 490  
Db 421 GAAGTGGCTTTCGGGCTGGTGTGCGCAACTTTCGAAACAGATGCTGACAGTCAAGCCGG 480  
QY 491 AGCCACAGGCGAGATGGTGACCAACCAACCCCTGATCAGGACAGCAAGAAAGATGGTG 550  
Db 481 TCCACCGCTCAATGGTTCACCAACCAACCTCGCTGATTAGACATGAATTCGATGGTT 540  
QY 551 CTGCGCAGCACACCGCCAAAGCCATGGAGCAGATGGCGGCGAGCAGCAGCGCGCC 610  
Db 541 CTAGCATCAACTACAGCCAAAGCAATGGAAACAAATGGCGGAGCTCCGAGCAGGCTGCC 600  
QY 611 GAGGCCATGAGGTGGCGCAGCGCAGGCGAGGAGATGGTGAGGCCATGAGSACCATCGGC 670  
Db 601 GAGGCGATGAGGTGGCGTCCAGGCCAGACAGATGGTACAGGCTATGAGAACTATCGGT 660  
QY 671 ACCCACCCAGCAGCAGCGCGCTCGAAGAACGACCTGTGAGAGAACCTTCAGGCGCTAC 730  
Db 661 ACGACCCAAAGTCTTCAGCTGGGCTGAAGATGATCTTCTTGAGAACCTTCAGGCGCTAC 720  
QY 731 CAGAAGCGCATGGCGCTGCAGATGACGCGCTTTCAA 765  
Db 721 CAAAAGCGGATGGCGCTCCAGATGACAGAGATTTAA 755

## RESULT 8

US-11-131-479-3  
; Sequence 3, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131.479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: Influenza A virus  
US-11-131-479-3

Query Match 62.5%; Score 484.6; DB 12; Length 1027;  
Best Local Similarity 76.8%; Pred. No. 8e-96;  
Matches 592; Conservative 0; Mismatches 179; Indels 0; Gaps 0;  
QY 1 AGATCTAAAGATGAGCTGCTGACCGAGGTGGAGACCTAGCTGTGAGCATCATCCCCAG 60  
Db 16 ATATTGAAGATGAGTCTTCTTAACCGAGGTGCGAAACGTAGCTACTCTCTATCATCCCC 75  
QY 61 CGGCCCCCTGAAGCCGAGATCGCCAGAGCTGGAGAGCTGTTCGCCGCAAGAACAC 120  
Db 76 AGGCCCCCTCAAGCCGAGATCGCACAGACTTTGAAGATGTCTTTGAGGGAAGAAC 135  
QY 121 CGACTTGAGGTGCTGATGGAGTGGCTGAAGACAGGCCCCATCTCGAGCCCCCTGACCAA 180

Db 136 TGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAA 195  
Qy 181 GGGCATCTCTGGGCTTCGTGTTCACTCCCTGACCGTCCAGAGCGCGCCTTGACGCGCG 240  
Db 196 GGGGATTTTAGGATTTGTGTTTCACTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 255  
Qy 241 CCGCTTCGTGAGAAAGCCCTGAACGGCAACGGCGACCCCAACAAATGAGCAAGGCGGT 300  
Db 256 ACGCTTTTTCAAAATGCCCTTAATGGGAACGGGGATCCAAATTAACATGAGCAAAAGCAGT 315  
Qy 301 GAACCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCACGGCGCCCAAGGAGATCACGCT 360  
Db 316 TAAACTGTATAGGAAGCTCAAGAGGGAGATTAACAATTCATGGGGCCCAAGAAATCTCACT 375  
Qy 361 GAGCTACAGCGCGCGGCTTCGGCCAGCTGCATGGGCTGTATACCAACAGGATGGGCGC 420  
Db 376 CAGTTATTCTGCTGTCACITTCAGTTGATGGGCTCATATACAAACAGGATGGGCGC 435  
Qy 421 CGTACACCGAGTGGGCTTCGGCGCTGGTGTGGCCACCTGCGAGCAGATGGCGGACAG 480  
Db 436 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTTGCTGACTC 495  
Qy 481 CCAGCACCGCACAGGCGAGATGGTGACCAACCAACCCCTGTATCAGGACGACGAGAA 540  
Db 496 CCAGCATGGTCTCATAGGCAAAATGGTGACAAACCAATCCACTAATCAGACATGAGAA 555  
Qy 541 CAGGATGGTGTGGCCAGCACACCGCCAGGCGCATGGAGCAGATGGCGGCGCAGACGGA 600  
Db 556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGTCCAGTGA 615  
Qy 601 GCAGGCGCGAGCGCATGGAGGTGGCCAGCCAGGCGCAGGAGATGGTGAGGCGCATGAG 660  
Db 616 GCAAGCAGCAGAGGCGCATGGAGGTGGTGTAGTCAAGCTAGACAAATGGTGCAAGCGATGAG 675  
Qy 661 GACCATGGGACCCACCCAGCAGCGCGGCTGAAGAACGACCTGTGGAGAACCT 720  
Db 676 AACCATTTGGGACTCATCTAGCTCAGTGTGGTCTGAAAATGATCTTCTTGAATTT 735  
Qy 721 GCAGGCTTACCAAGCGCATGGGCGTGCAGATGCGCGCTTCAAGTGAAC 771  
Db 736 GCAGGCTTATCAGAAACGAATGGGGTGCAGATGCAACGGTTCAAGTATC 786

RESULT 9  
US-11-131-479-45  
; Sequence 45, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 45  
; LENGTH: 1305  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Influenza A Virus M1 Fused to Synthetic HbCag  
US-11-131-479-45

Query Match 61.4%; Score 476; DB 12; Length 1305;  
Best Local Similarity 76.9%; Pred. No. 5, 7e-94;  
Matches 581; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

Qy 11 ATGAGCCTGCTACGAGGTGGAGACCTAGCTGCTGAGCATCATCCCGAGCGCCCTCG 70  
Db 1 ATGAGTCTTTCTAACCGAGGTGCAAACTAGCTACTCTCTATCATCTCCGTGAGCGCCCTC 60  
Qy 71 AAGGCCGAGATCCCGCAGAGGTGGAGGACGTGTTCGCCGGCAAGAACACCGGACCTGGAG 130  
Db 61 AAAGCCGAGATCCACAGAGACTTGAAGATGTCTTTGAGGGAAGAACACTGATCTTGAG 120  
Qy 131 GTGCTGATGGAGTGGCTGAAGACAGGCCCATCTTGAGCCCCCTGACCAAGGGGCACTCG 190  
Db 121 GTTCTCATGGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAAGGGGATTTTA 180  
Qy 191 GGGCTTGCTTACCTGTACCTGTGCCAGGAGCGGGCTGTGAGCGCCCGCTTCGTG 250  
Db 181 GGAATTTGTGTTACGCTCACCGTCCAGTGAAGCGGAGGACTGCAGCGGTAGACGCTTTGTC 240  
Qy 251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACAATGGAACAAGGCCGTGAAGCTGTAC 310  
Db 241 CAAATGCCCTTAATGGGAACGGGGATCCAAATTAACATGGAACAAGCAGTTAAACTGTAT 300  
Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCAGCGGCCCAAGGAGATCAGCCTGAGCTACAGC 370  
Db 301 AGGAAGCTCAAGAGGGAGATAACATTCATGGGGCCAAAGAAATCTCACTCAGTTATCT 360  
Qy 371 GCGGGCGCCTGCGCAGCTGCTATGGGCTGTATCAACAGGATGGGCGCCGTGACCC 430  
Db 361 GCTGGTGCACTTGCAGTTGTATGGGCTCATATACAACAGGATGGGGGCTGTGACCACT 420  
Qy 431 GAGGTGGCTTTCGGCTGTGGTGTGGCCACTGCGAGCAGATCGCGGACAGCCAGCACCGC 490  
Db 421 GAATGGCAATTTGGCTGGTATGTGCAACTGTGGAACAGATTTGCTGACTCCAGCATCGG 480  
Qy 491 AGCCACAGGCGAGATGGTGACCAACCAACCCCTGATCAGGACGAGAACAGAGATGGT 550  
Db 481 TCTCATAGGCAATGGTGACCAACCAATCCACTAATCAGACATGAGAAACAGAAATGGTT 540  
Qy 551 CTGCGCAGACCAACCGCCAGGCGCATGGAGCAGATGGCGGCGCAGCAGCGAGCGCGCC 610  
Db 541 TTAGCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCGAGTGAGCAAGCAGCA 600  
Qy 611 GAGGCCATGAGGTGGCCAGCGCAGGCGCAGATGGTGCAGGCGCATGAGGACCATCGGC 670  
Db 601 GAGGCCATGAGGTGGTGTAGTGTAGGCTAGACAAATGGTGCAGGGATGAGAACCATTTGG 660  
Qy 671 ACCCACCCAGCAGCAGCGCGCTGGAAGAACGACTGTCTGGAGAACCTGCGAGGCTTAC 730  
Db 661 ACTCATCTAGTCCAGTGTGGTCTGAAAAATGATCTTCTTGAATAATTTGCGAGGCTAT 720  
Qy 731 CAGNAGGCGATGGCGTGCAGATGCGCGCTTCAAG 766  
Db 721 CAGAAACGAATGGGGTGCAGATGCAACGGTTCAAG 756

RESULT 10  
US-11-155-478A-131  
; Sequence 131, Application US/11155478A  
; Publication No. US2006001410A1  
; GENERAL INFORMATION:  
; APPLICANT: Boivin, Guy  
; APPLICANT: UNIVERSITE LAVAL  
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING  
; FILE REFERENCE: 6013-148US  
; CURRENT APPLICATION NUMBER: US/11/155,478A  
; CURRENT FILING DATE: 2005-06-20  
; PRIOR APPLICATION NUMBER: CA 2,411,264  
; PRIOR FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: CA 2,418,004  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994  
; PRIOR FILING DATE: 2003-12-19  
; NUMBER OF SEQ ID NOS: 174

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 987
; TYPE: DNA
; ORGANISM: human Influenza A virus
; FEATURE:
; NAME/KEY: Gene
; LOCATION: (1)...(987)
; OTHER INFORMATION: human Influenza A virus
; OTHER INFORMATION: strain A/Charlottesville/31/95 (H1N1)
; OTHER INFORMATION: accession number AF398876
US-11-155-478A-131

Query Match          59.8%; Score 463.4; DB 12; Length 987;
Best Local Similarity 75.6%; Pred. No. 3e-91;
Matches 575; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

Qy 11 ATGAGCTGTGACCGAGGTGGAGACTTACGTGTGAGCATATCCCGAGGCGCCCTG 70
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 ATGAGCTTCTTAACCGAGGTGGAACGTACGTCTCTATCGTCCCGTCAGGCGCCCTC 60
Qy 71 AAGCCGAGATCGCCAGAGCTGGAGACGTGTTCCGCGCAAGAACACCGACTGGAG 130
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 AAGCCGAGATCGCCAGAGACTTGAAGATGTTCTTGTGGAAGAACACCGACTTGGAG 120
Qy 131 GTGCTGATGGAGTGGCTCAAGACAGGCGCCATCTGTGAGCCCTTGACCAAGGGATCCTG 190
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 GCTCTCATGGAGTGGCTTAAAGACAGACCGATCTCTGTCACCTCTGACTTGAAGGGATTTTA 180
Qy 191 GGTCTTGTTTCACTGACCGTCCAGCGAGCGCGCTTGCAGCGCGCGCTTCTG 250
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 GGAATTTGTTTCACTGACCGTCCAGTGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 240
Qy 251 CAGAACGCTTGAAGGAGATCACTTCCAGCGCGCAAGGAGATCAGCTCAGCTTACAGC 310
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 CAAATATGCTTAAATGGGAATGGGGATCCAAATTAACATGGAAGCAGACGATTTAAATCTGAT 300
Qy 311 AGGAAGCTTGAAGGAGATCACTTCCAGCGCGCAAGGAGATCAGCTCAGCTTACAGC 370
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 AGAAGCTTGAAGGAGATCACTTCCAGCGCGCAAGGAGATCAGCTCAGCTTATTTCT 360
Qy 371 GCGGCGCTTGGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 GCTGTCACCTTGGCGAGTGGCTTATGAGCAATGGCTGATGAGCAATGGCTGATGAGCAATGGCT 420
Qy 431 GAGGTGCTTGGCGAGTGGCTTATGAGCAATGGCTGATGAGCAATGGCTGATGAGCAATGGCT 490
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
421 GAAATGCTTGGCGAGTGGCTTATGAGCAATGGCTGATGAGCAATGGCTGATGAGCAATGGCT 480
Qy 491 AGCCACAGGAGATGGTGACCAACCAACCTCTGATCAGGCAAGGAGATCAGCTGAGCTACAGC 550
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
481 TCTCATAGGCAATGGTGAGCAACCAATCCATTAATAGGCAATGAGCAATGATGATGATGATGAT 540
Qy 551 CTGGCGAGCAGCAGCGCAAGGCAATGGAGCAGATGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 610
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
541 CTGGCGAGCAGCAGCAGTAAAGCTATGAGCAATGGCTGATGAGCAATGGCTGATGAGCAATGGCT 600
Qy 611 GAGGCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 670
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
601 GAGGCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Qy 671 ACCCACCCAGCAGCGCGCTGAAGAACCGACCTGCTGGAGAACCGACCTGCTGGAGAACCGACCT 730
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
661 ACTCATCTAGCTTAGCAGCTGGCTGAAGAACCGACCTGCTGGAGAACCGACCTGCTGGAGAACCG 720
Qy 731 CAGAAGCGCATGGGCGTGCAGATGAGCGCTTCAAGTGAAC 771
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
721 CAGAAACGAATGGGGTGCAGATGCAACGATTTCAAGTATC 761

RESULT 11
US-11-131-479-60
; Sequence 60, Application US/11131479
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Db 661 ACTCATCTAGCTCCAGTGTGGTCTAAAGATGATCTTTGAAATTTGCAGACCTAT 720  
Qy 731 CAGAAAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771  
Db 721 CAGAAACGAATGGGGTGCAGATGCAACGATTCAAGTGACC 761

## RESULT 12

US-11-131-479-95  
; Sequence 95, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 95  
; LENGTH: 4822  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VR4764, Ligation of VR4756 RV-Sali into VR10682 RV  
US-11-131-479-95

Query Match 59.0%; Score 457; DB 12; Length 4822;  
Best Local Similarity 75.0%; Pred. No. 6.8e-90;  
Matches 571; Conservative 0; Mismatches 190; Indels 0; Gaps 0;  
Qy 11 ATGAGCCTGTGACCGAGGTGGAGACCTACCTGCTGTGAGCATCATCCCCAGCGGCCCTG 70  
Db 814 ATGAGCCTTCTAACCGAGGTGGAACGATGTCTCTATCGTTCCATCAGGCCCTC 873  
Qy 71 AAGCCGAGATCGCCAGAGCTGGAGGACGTGTTCGCCGCGCAAGAACACCGACCTGGAG 130  
Db 874 AAGCCGAAATCGCGCAGAGACTTTGAAGATGTCTTTGCTGGGAAAAACACAGATCTTGA 933  
Qy 131 GTGCTGATGGAGTGGCTGAACAGCAGGCCCATCTGTAGCCCTTGACCAAGGGCATCTG 190  
Db 934 GCTCTCATGGAAATGGCTTAAGACAAAGACCAATCTCTGTCACCTCTGACTAAGGGGATTTG 993  
Qy 191 GGCTTGTGTTTCCACCTGACCGTGCACGAGCGCGCCCTGCGAGCGCGCGCTTCGTG 250  
Db 994 GGGTTGTGTTTCCACCTGACCGTGCACGAGTGCAGGAGTGCAGCGTAGCGCTTTGTC 1053  
Qy 251 CAGAAAGCCCTGAAAGCGCAAGCGGACCCCAACACATGGAAGAGCGCGTGAAGCTGTAC 310  
Db 1054 CAAAATGCCCTCAATGGGAATGGGGATCCAAATAACATGAGACAGACGAGTAAACTATAT 1113  
Qy 311 AGGAAGCTGAAGAGGAGATCACCTTCCACGCGCCAGAGGAGATCAGCTGAGCTACAGC 370  
Db 1114 AGAAAACCTTAAGAGGAGATTTACATTTCCATGGGGCCAAAGAAATAGCACTCAGTTATTCT 1173  
Qy 371 GCCGCGCCCTTGGCAGCTGATGGGCTGTATCTACAAACAGATGGGCGCGCTGACCAACC 430  
Db 1174 GCTGGTGACTTGGCAGTTGATGGGCTCTATATACACAGATGGGGGCTGAACCACT 1233  
Qy 431 GAGTGGCTTGGCCTGGTGTGGCCACTCTGCGAGAGAGATGCGCGACAGCGACCGC 490  
Db 1234 GAAGTGGCTTGGGCTGGTATGTGCAACATGTGAACAGATTTGCTGACTCCCGACAGG 1293  
Qy 491 AGCCACAGCGAGATGGTGAACCAACCAACCCCTGATCAGGACAGAGACAGGATGGT 550

Db 1294 TCTCATAGGCABAATGGTGGCAACCAACTCCATTAAATAGGCATGAGAACAGATGGTT 1353  
Qy 551 CTGGCAGACACCAACCGCAAGGCCATGGAGCAGATGGCCGGCAGCAGCAGCAGCGCC 610  
Db 1354 TTGGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGGATCAAGTGAAGCGCAGCG 1413  
Qy 611 GAGGCCATGGAGTGGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGC 670  
Db 1414 GAGGCCATGGAATTGTCTAGTCAGGCCAGGCAATGTGCGGCAATGAGGCCATTTGGG 1473  
Qy 671 ACCCAGCCAGCAGCAGCGCGCCCTGAAGAACGACCTGTGTGAGAACCTGCGAGCGCTAC 730  
Db 1474 ACTCATCTAGTCCAGTGTCTTAAAGATGATCTTCTTGAATAATTTGCAGACCTAT 1533  
Qy 731 CAGAAAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771  
Db 1534 CAGAAACGAATGGGGTGCAGATGCAACGATTCAAGTGACC 1574

## RESULT 13

US-11-131-479-101  
; Sequence 101, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 101  
; LENGTH: 5161  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VR4770, M2 Insert Replacing WNv Insert in VR6430  
US-11-131-479-101

Query Match 59.0%; Score 457; DB 12; Length 5161;  
Best Local Similarity 75.0%; Pred. No. 6.8e-90;  
Matches 571; Conservative 0; Mismatches 190; Indels 0; Gaps 0;  
Qy 11 ATGAGCCTGTGACCGAGGTGGAGACCTACCTGCTGTGAGCATCATCCCCAGCGGCCCTG 70  
Db 1147 ATGAGCCTTCTAACCGAGGTGGAACGATGTCTCTATCGTTCCATCAGGCCCTC 1206  
Qy 71 AAGCCGAGATCGCCAGAGCTGGAGGACGTGTTCGCCGCGCAAGAACACCGACCTGGAG 130  
Db 1207 AAGCCGAAATCGCGCAGAGACTTTGAAGATGTCTTTGCTGGGAAAAACACAGATCTTGA 1266  
Qy 131 GTGCTGATGGAGTGGCTGAAAGACAGGCCCATCTGTAGCCCTTGACCAAGGGCATCTG 190  
Db 1267 GCTCTCATGAAATGGCTTAAGACAAAGACCAATCTGTCACTCTGACTAAGGGGATTTG 1326  
Qy 191 GGCTTGTGTTTCCACCTGACCGTGCAGCGCGCGCTGCGAGCGCGCGCTTCGTG 250  
Db 1327 GGGTTTGTGTTTACGCTCAGCGTGCAGCGTGCAGCGCGCGAGTGCAGCGCTTTGTC 1386  
Qy 251 CAGAAAGCCCTGAAAGCGCAAGCGGCCCAACCAACATGACAGAGCGCGTGAAGCTGTAC 310  
Db 1387 CAAAATGCCCTCAATGGGAATGGGGATCCAAATACATGACAGACAGATTAACATATAT 1446  
Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCAGCGCGCCAGAGGAGATCAAGCTGAGTACAGC 370  
Db 1447 AGAAAACCTTAAGAGGAGATTTACATTTCCATGGGGCCAAAGAAATAGCACTCAGTTATTCT 1506

Qy 371 GCGGCGCCTGGCCAGCTGATGGCCCTGATCTACAAACAGATGGGCGCGCTGACCACC 430  
Db |||||  
1507 GCTGGTGACATTGCCAGTTGCATGGGCTCATATACACAGATGGGGGCTGTAACTACT 1566  
Qy 431 GAGGTGGCTTGGGCTGGTGGCCACCTGCGGAGCAGATGCGGACAGCAGCAGCCG 490  
Db |||||  
1567 GAAAGTGGCTTGGGCTGGTATGTGCAACATGTGAACAGATTGCTGACTCCAGCAGCAGG 1626  
Qy 491 AGCCACAGCAGATGGTGACACCAACCAACCCCTGATCAGGACGAGAACAGGATGGT 550  
Db |||||  
1627 TCTATAGGCAATGGTGGCAACCAACCAATCCATTAATAGGCATGAGAACAGATGGT 1686  
Qy 551 CTGGCCAGCACACCGCCCAAGCCCATGAGCAGATGGCGGCGCAGCAGCAGCAGCCGCC 610  
Db |||||  
1687 TTGGCCAGCACTACAGCTAAGCTATGGACCAATGGCTGATCAAGTGAGCAGCAGCG 1746  
Qy 611 GAGGCCATGAGGTGGCCAGCCAGCCAGGAGATGGTGAGGCAATGAGAACCATGGC 670  
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1747 GAGGCCATGAAATTTGCTAGTCAGGCCAGGCAATGGTGAGGCAATGAGAGCCATTGGG 1806  
Qy 671 ACCACCCAGCAGCAGCGCGGCTGAGAACGACCTGCTGGAGAACCTGCAGGCCCTAC 730  
Db |||||  
1807 ACTCATCTAGCTCCAGTGGCTGCTAAAGATGATCTTCTTGAAATTTTCAGACCTAT 1866  
Qy 731 CAGAAGCGCATGGGCGTGCAGATGAGCGCTTCAAGTGAAC 771  
Db |||||  
1867 CAGAAACGAATGGGGTGCAATGCAACGATTCAGTGACC 1907

## RESULT 14

US-11-131-479-91  
; Sequence 91, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 91  
; LENGTH: 5398  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VR4756, Ligation of Segment7 into VR10551  
US-11-131-479-91

Query Match 59.0%; Score 457; DB 12; Length 5398;  
Best Local Similarity 75.0%; Pred. No. 6.8e-90;  
Matches 571; Conservative 0; Mismatches 190; Indels 0; Gaps 0;  
Qy 11 ATGAGCTGCTGACCGAGGTGAGACCTACCTGCTGAGCATATCCCGAGCGGCCCTG 70  
Db |||||  
1652 ATGAGCTTCTAACCGAGGTGAAACGATATGTTCTCTATGTTCCATGAGCCCCCTC 1711  
Qy 71 AAGGCCGAGATCGCCAGAGCTGGAGGACGTGTTGCGCGCAAGAACACCGACCTGGAG 130  
Db |||||  
1712 AAAGCCGAATCGCGCAGACTTGAAGATGCTTTGCTGGGAAAACACAGATCTTGAG 1771  
Qy 131 GTGCTGATGGATGGCTGAAGACAGGCGCCATCTCTGAGCCCTCTGACCAAGGGATCTGT 190  
Db |||||  
1772 GCTCTCATGGAATGGCTAAAGACAAAGCAATCTCTGTCACCTCTGCTAAAGGGATTTTG 1831

Qy 191 GGCTTCGTGTTTACCTGACCGTCCAGCAGAGCGCGCTGACGCGCGCGCTTCGTG 250  
Db |||||  
1832 GGGTTTGTGTTTACGCTCACCGTCCAGTGCAGGAGGACTGCAGCGTAGACGCTTTGTC 1891  
Qy 251 CAGAACGCCCTGAAGCGCAACCGGACCCCAACAAATGGAACAAGGCGCGTAGCTGAC 310  
Db |||||  
1892 CAAATGCCCTCAATGGGATGGGATCCAAATTAACATGGAACAGAGCAAGTTAAACTATAT 1951  
Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCAGGGCCCAAGGAGATCAGCTTCAGCTTACAGC 370  
Db |||||  
1952 AGAAAATTAAAGAGGAGATTAATTCATGGGGCCAAAGAAATAGCACTCAGTTATTCT 2011  
Qy 371 GCCGCGCCCTGGCCAGCTGCATGGGCTGATCTACAAACAGATGGGCGCGCTGACCAACC 430  
Db |||||  
2012 GCTGGTGCACTTGCAGTTGCATGGGCTCATATAACAACAGAAATGGGGCTGTAACTACT 2071  
Qy 431 GAGTGGCTTGGCCCTGGTGTGGCCACCTGCGAGCAGATGCGCGCAGCAGCAGCAGCCG 490  
Db |||||  
2072 GAAGTGGCTTGGCCCTGGTATGTGCAACATGTGAACAGATTTGCTGACTCCAGCACAGG 2131  
Qy 491 AGCCACAGGAGATGGTGACCCACCACCAACCCCTGATCAGGCACGAGAACAGATGGT 550  
Db |||||  
2132 TCTCATAGGCAATGGTGGCAACCAATCATTAATAGGCATGAGAACAGATGGT 2191  
Qy 551 CTGGCCAGCACCAACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCAGCCGCC 610  
Db |||||  
2192 TTGGCCAGCACTACAGCTAAGGCTATGAGCAATGCTGGATCAAGTGAGCAGCAGCAGC 2251  
Qy 611 GAGGCCATGAGGTGGCCAGCAGCAGCAGCAGATGGTGAGGCCATGAGGACCATGGC 670  
Db |||||  
2252 GAGGCCATGGAATTTGCTAGTCAGGCCAGGCAATGGTGGCAGCAATGAGAGCCATTGGG 2311  
Qy 671 ACCCAGCCAGCAGCAGCGCGCTGAGAACGACCTGCTGGAGAACCTTCAGGCGCTTAC 730  
Db |||||  
2312 ACTCATCTAGCTCCAGTGGTCTAAAGATGATCTTCTTGAATAATTTTCAGACCTAT 2371  
Qy 731 CAGAAGCGCATGGGCGTGCAGATGAGCGCTTCAAGTGAAC 771  
Db |||||  
2372 CAGAAACGAATGGGGTGCAATGCAACGATTCAGTGACC 2412

## RESULT 15

US-11-131-479-97  
; Sequence 97, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 97  
; LENGTH: 7798  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VR4766, Ligation of Seg7 into VR4762  
US-11-131-479-97

Query Match 59.0%; Score 457; DB 12; Length 7798;  
Best Local Similarity 75.0%; Pred. No. 6.7e-90;  
Matches 571; Conservative 0; Mismatches 190; Indels 0; Gaps 0;  
Qy 11 ATGAGCTGCTGACCGAGGTGGAGACCTACCTGCTGAGCATATCCCGAGCGGCCCTG 70

[illegible]

Search completed: March 21, 2006, 01:31:30  
Job time : 357.36 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model  
Run on: March 20, 2006, 23:02:13 ; Search time 171.124 Seconds  
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8767.110 Million cell updates/sec

Title: US-10-729-830-4  
Perfect score: 844  
Sequence: 1 agactaaagatggcgctca.....agcgcttaagtgaactagt 844

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ins/5 COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ins/6A COMB.seq:\*  
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8: /cgn2\_6/ptodata/1/ins/RE COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 479.6 | 56.8        | 4023   | 3     | US-08-809-513A-8  |
| 2          | 479.6 | 56.8        | 6802   | 3     | US-08-809-513A-6  |
| 3          | 477.6 | 56.6        | 1023   | 3     | US-09-506-286B-1  |
| 4          | 477.6 | 56.6        | 1023   | 3     | US-09-762-861B-1  |
| 5          | 477.6 | 56.6        | 1023   | 3     | US-10-065-133A-1  |
| 6          | 477.6 | 56.6        | 1023   | 3     | US-10-434-811A-1  |
| 7          | 477.4 | 56.6        | 816    | 3     | US-09-311-784A-13 |
| 8          | 474.8 | 56.3        | 1023   | 3     | US-09-506-286B-4  |
| 9          | 474.8 | 56.3        | 1023   | 3     | US-09-762-861B-4  |
| 10         | 474.8 | 56.3        | 1023   | 3     | US-10-065-133A-4  |
| 11         | 474.8 | 56.3        | 1023   | 3     | US-10-434-811A-4  |
| 12         | 474.2 | 56.2        | 756    | 3     | US-09-506-286B-3  |
| 13         | 474.2 | 56.2        | 756    | 3     | US-09-762-861B-3  |
| 14         | 474.2 | 56.2        | 756    | 3     | US-10-065-133A-3  |
| 15         | 474.2 | 56.2        | 756    | 3     | US-10-434-811A-3  |
| 16         | 471.4 | 55.9        | 756    | 3     | US-09-506-286B-6  |
| 17         | 471.4 | 55.9        | 756    | 3     | US-09-762-861B-6  |
| 18         | 471.4 | 55.9        | 756    | 3     | US-10-065-133A-6  |
| 19         | 471.4 | 55.9        | 756    | 3     | US-10-434-811A-6  |
| 20         | 465.2 | 55.1        | 1027   | 6     | PCT-US95-12357A-3 |
| 21         | 79.2  | 9.4         | 2403   | 2     | US-08-471-033-30  |
| 22         | 79.2  | 9.4         | 2403   | 2     | US-08-471-044-30  |
| 23         | 79.2  | 9.4         | 2403   | 2     | US-08-463-483A-30 |
| 24         | 79.2  | 9.4         | 2403   | 2     | US-08-471-046A-30 |

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| 25 | 79.2 | 9.4 | 2403 | 2 | US-08-470-566B-30 | Sequence 30, Appl |
| 26 | 79.2 | 9.4 | 2403 | 2 | US-08-838-219B-7  | Sequence 7, Appl  |
| 27 | 79.2 | 9.4 | 2403 | 2 | US-08-469-334-30  | Sequence 30, Appl |
| 28 | 79.2 | 9.4 | 2403 | 3 | US-09-300-529-30  | Sequence 30, Appl |
| 29 | 79.2 | 9.4 | 2403 | 3 | US-09-233-336A-7  | Sequence 7, Appl  |
| 30 | 79.2 | 9.4 | 2403 | 3 | US-09-233-752A-7  | Sequence 7, Appl  |
| 31 | 79.2 | 9.4 | 2403 | 3 | US-09-402-036-7   | Sequence 7, Appl  |
| 32 | 79.2 | 9.4 | 2403 | 3 | US-09-904-226-7   | Sequence 7, Appl  |
| 33 | 77.8 | 9.2 | 1387 | 3 | US-09-475-515-34  | Sequence 34, Appl |
| 34 | 77.8 | 9.2 | 1944 | 3 | US-09-475-515-37  | Sequence 37, Appl |
| 35 | 77.8 | 9.2 | 1944 | 3 | US-09-475-515-38  | Sequence 38, Appl |
| 36 | 77.8 | 9.2 | 1944 | 3 | US-09-475-515-40  | Sequence 40, Appl |
| 37 | 77.8 | 9.2 | 1944 | 3 | US-09-475-515-43  | Sequence 43, Appl |
| 38 | 77.8 | 9.2 | 1944 | 3 | US-09-475-515-46  | Sequence 46, Appl |
| 39 | 77.8 | 9.2 | 2466 | 3 | US-09-475-515-49  | Sequence 49, Appl |
| 40 | 77.8 | 9.2 | 4608 | 3 | US-09-475-515-76  | Sequence 76, Appl |
| 41 | 77.6 | 9.2 | 2241 | 2 | US-08-838-219B-20 | Sequence 20, Appl |
| 42 | 77.6 | 9.2 | 2241 | 3 | US-09-233-336A-20 | Sequence 20, Appl |
| 43 | 77.6 | 9.2 | 2241 | 3 | US-09-233-752A-20 | Sequence 20, Appl |
| 44 | 77.6 | 9.2 | 2241 | 3 | US-09-402-036-20  | Sequence 20, Appl |
| 45 | 77.6 | 9.2 | 2241 | 3 | US-09-904-226-20  | Sequence 20, Appl |

ALIGNMENTS

RESULT 1

US-08-809-513A-8  
; Sequence 8, Application US/08809513A  
; Patent No. 6524588  
; GENERAL INFORMATION:  
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette  
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a  
; TITLE OF INVENTION: Method  
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS  
; STREET: 660 White Plains Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591-5144  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage  
; COMPUTER: Gateway Pentium II  
; OPERATING SYSTEM: Windows 98  
; SOFTWARE: Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,513A  
; FILING DATE: 24-MAR-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/03663  
; FILING DATE: 18-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94115505.3  
; FILING DATE: 30-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurt G. Briscoe  
; REGISTRATION NUMBER: 33,141  
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 332-1700  
; TELEFAX: (914) 332-1844  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4023 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO



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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus, RNA sequence
; INDIVIDUAL ISOLATE: pHL1490
US-08-809-513A-8

Query Match      56.8%; Score 479.6; DB 3; Length 4023;
Best Local Similarity 77.0%; Pred. No. 1.8e-80;
Matches 584; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

Qy 83 AGCTGCTGACCGAGGTGGAGACTACGTGCTGAGCATATCCCGAGCGCCCTCGAAG 142
Db |||||
Qy 21 AGTCTTCTAACCGAGGTGGAACGTAGTCTCTATCATCCGTCAGGCCCTCAAA 80
Db |||||
Qy 143 GCCGAGATCGCCACGAGCGTGGAGAGCGTGTTCGCCGCAAGAACACCGACCTGGAGGTG 202
Db |||||
Qy 81 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTCAGGGAAGAACCGATCTTGAGGTT 140
Db |||||
Qy 203 CTGATGAGTGGCTGAAGACAGAGCCCATCTCTAGAGCCCTGACCAAGGGATCTCTGGC 262
Db |||||
Qy 141 CTCATGGAATGGCTAAAGACAGACCAATCTGTCTGACTTAAGGGGATTTTAGGA 200
Db |||||
Qy 263 TTCGTGTTTCAACCTGACCGTCCAGCGAGCGCGCTGACAGCGCCCGCTTCGTGCAG 322
Db |||||
Qy 201 TTTGTGTTTCACTACCGTCCAGTGCAGGAGACTGACGCTAGACGCTTGTGTCAA 260
Db |||||
Qy 323 AACGCCCTGAACGGCAACCGCGACCCCAACAAATGACAGAGCGCGTGAAGCTGTACAGG 382
Db |||||
Qy 261 AATGCCCTTAATGGGAACGGGATCCAAATAAATGACAAAGCAGTTAACTGTATAGG 320
Db |||||
Qy 383 AAGCTGAAGAGGGAGATCACCTTCCAGCGGCCAAGGAGATCAGCCTGAGGTACAGGCC 442
Db |||||
Qy 321 AAGCTCAAGAGGGAGATAAATTCATGGGGCCAAAGAAATCTCACTCAGTTATTCGCT 380
Db |||||
Qy 443 GGGCCCTGGCCAGCTGATGGGCTGATCTTACAAAGAGTGGCGCGTGACCAACCGAG 502
Db |||||
Qy 381 GGTGCATTTGCCAGTTGTATGGGCTCATATACAAAGGATGGGGGTGTGACCACTGAA 440
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Qy 503 GTGGCCTTGGGCTTGGTGTGGCCACCTCGAGCAGATTCGCCGACAGCAGCCGACG 562
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Qy 441 GTGSCATTTGGCCCTGGTATGTGCAACCTGTGAACAGATTTGCTGACTCCAGCATCGTCT 500
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Qy 501 CATAGGCAAAATGGTGACAAACCAACCCACTAATACAGATGAGAACAGAAATGTTTAA 560
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Qy 623 GCCAGCACCGCCAGAGGCGCATGGAGCAGATGGCCGACAGCAGGAGCGCCGCGAG 682
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Qy 561 GCCAGCACTACAGTAAAGGCTATGGAGCAATGGCTGATCGATGAGCAAGCAGAGAG 620
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Qy 683 GCCATGAGGTGGCCAGCCAGGCGCAGGAGATGTGTGAGGCGCATGAGGACCATCGGCAAC 742
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Qy 621 GCCATGAGGTGTGTAGTCAGGCTAGGCAATGGTGCAAGGATGAGAACCATTTGGGACT 680
Db |||||
Qy 743 CACCCAGCAGCAGCGCGGCTGAAGACACCTCTGTGGAGACCTGTCAGGCGCTACAG 802
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Qy 681 CATCTAGCTCAGTGTGCTGTGAAAATGCTCTCTTTGAAAATTTTGCAGGCGCTATCAG 740
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Qy 803 AAGGCGATGGCGTGCAGATCAGCGCTTCAAGTGAAC 840
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Qy 741 AAACGAATGGGGTGCAGATGCAAGGTTCAAGTGATC 778
Db |||||

RESULT 2
US-08-809-513A-6
; Sequence 6, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Gateway Pentium II
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,513A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/BP95/03663
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94115505.3
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6802 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus, RNA sequence
; INDIVIDUAL ISOLATE: pHL1191
US-08-809-513A-6

Query Match      56.8%; Score 479.6; DB 3; Length 6802;
Best Local Similarity 77.0%; Pred. No. 1.9e-80;
Matches 584; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

Qy 83 AGCTGCTGACCGAGGTGGAGACTACGTGCTGAGCATATCCCGAGCGCCCTCGAAG 142
Db |||||
Qy 41 AGTCTTCTAACCGAGGTGGAACGTAGTCTCTATCATCCGTCAGGCCCTCAAA 100
Db |||||
Qy 143 GCCGAGATCGCCACGAGGTGGAGAGCGTGTTCGCCGCAAGAACACCGACCTGGAGGTG 202
Db |||||
Qy 101 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTCAGGGAAGAACCGATCTTGAGGTT 160
Db |||||
Qy 203 CTGATGAGTGGCTGAAGACAGCGCCCATCTGAGCCCCCTGACCAAGGSCATCTTGGC 262
Db |||||
Qy 161 CTATGGAATGGTGAAGACAAAGCAACCAATCTGTCACTTAAGGGGATTTTAGGA 220
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Qy 263 TTGCTGTTTCACTGACCGTGCAGCGAGCGGCGCTGCAGGCGCCGCTTCGTGCAG 322
Db |||||
Qy 221 TTTGTGTTTCACTGACCGTGCAGCGGCGCTGCAGGAGGACTGCGAGCTGTGTCAA 280
Db |||||
Qy 323 AACGCCCTGAACGGCAACCGCGACCCCAACAAATGAGCAAGGCGCTGGAAGCTGTACAGG 382
Db |||||
Qy 281 AATGCCCTTAATGGGAACGGGATCCAAATAAATGACAAAGCAGTTAACTGTATAGG 340
Db |||||
Qy 383 AAGCTGAAGAGGGAGATCACCTTCCAGCGGCCCAAGAGAGATCAGCCTGAGCTACAGGCC 442
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Qy 341 AAGCTCAAGAGGGAGATAAATTCATTTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCGCT 400
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Db 401 GGTGCACTTGCAGTTGTATGGGCTCATATACAACAGGATGGGGCTGTGACCACTGAA 460  
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Db 461 GTGGCAATTGGCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCAGCATCGGTCT 520  
Qy 563 CACAGGAGATGGTGAACACCAACCCCTGTATCAGGCGAGAGAACAGGATGGTGTG 622  
Db 521 CATAGGCAATGGTGACAAACCAACCAACCACTAATCAGACATGAGAACAGAAATGTTT 580  
Qy 623 GCCAGCACCGCCCAAGGCCATGGAGCAGATGGCCGCGCAGCAGGAGCGCCGCGAG 682  
Db 581 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCGAGTGAGCAAGCAGCAG 640  
Qy 683 GCCATGAGGTGGCCAGCCAGCCAGGCGAGATGGTGAGGCGCATGAGGACCATCGGCACC 742  
Db 641 GCCATGAGGTGGCTAGTCAAGCTAGGCAATGGTGCAAGCGATGAGAACCATTTGGGACT 700  
Qy 743 CACCCAGCAGCAGCGCGGCTGAAGAACGACCTGTCTGGAGAACCTGCAGGCGCTACCGAG 802  
Db 701 CATCTAGCTCAGTGTGCTGTAATAATGCTCTTCTTGAATAATTTGCGAGGCTATCAG 760  
Qy 803 AAGCGCATGGCGGTGCAGATGCGAGCGCTTCAAGTGAAC 840  
Db 761 AAACGAATGGGGTGCAGATGCAACGGTTCAAGTGATC 798

## RESULT 3

US-09-506-286B-1  
; Sequence 1, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth  
; FILE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US/09/506,286B  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION: At location 663, r = A or G; At amino acid  
; OTHER INFORMATION: location 213, Xaa = Val  
US-09-506-286B-1

Query Match 56.6%; Score 477.6; DB 3; Length 1023;  
Best Local Similarity 76.8%; Pred. No. 3.6e-80;  
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;  
Qy 83 AGCTGTCTGACCGAGGTGGAGACCTACGTGTGAGCATATCCCGAGCGGCCCTCGAAG 142  
Db 28 AGTCTTCTGACCGAGGTGCAACGTACGTTCTCTATCTGATCATCGGCCCTCTCAA 87  
Qy 143 GCCGAGATGCGCCAGAGCTGGAGAGCGTTTCGCGGCAAGAACACCGACCTCGAGGTG 202  
Db 88 GCCGAGATGCGCGAGAGCTTGAAGATGCTCTTTCGCGGAGAGAACCGATCTTGAAGCA 147  
Qy 203 CTGATGAGTGGCTGAAGACAGGCGCCATCTCTGAGCCCTGTGACAGGCGATCTCGGC 262  
Db 148 CTCATGGAATGGCTAAAGACAGACCAATCTCTGATCTGCTGACTAAGGGAATTTAGGA 207  
Qy 263 TTGCTGTTTCACTGACCGTGCCTCCAGCGAGCGCGCTGCGAGCGCGCGCTTCTGTCAG 322

Db 208 TTGCTATTCAGCTTACCGTGCAGTGCGGAGGACTGCGAGGTAGACGCTTTGTCAA 267  
Qy 323 AAGCCCTTGAACGCGACGCGACCCCAACCAACATGAGAACGCGCTGAAGCTGTACAGG 382  
Db 268 AATGCCCTTATGTGAAACGAGATCCAAACCAATGGACAGAGCAGTAAACCTGTACAGG 327  
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGAGAGATCAGCCCTGAGCTACAGGCC 442  
Db 328 AAGCTTAAAGAGAAATAACATTTCCATGGGCGCAAAAGAGGTGGCACTCAGCTATTCCACT 387  
Qy 443 GGGCCCTGCGCAGCTGCTGATGGGCTGATCTTAAACAGAGATGGGCGCGCTGACCAACCGAG 502  
Db 388 GGTGCACTAGCCAGCTGATGGGACTCATATACAACAGAAATGGGAATGTGACAACCGAA 447  
Qy 503 GTGGCTTCCGCTGGTGTGGCCACCTGCGAGCAGATCCCGACAGCCAGCAGCCGCGAGC 562  
Db 448 GTGGCATTTGGCTGGTATGCGCCACATGTGAACAGATCGCTGATTTCCAGCATCGATCT 507  
Qy 563 CACAGGAGATGGTGACCAACCAACCCCTGATCAGGCAACGAGACGAGATGGTGTG 622  
Db 508 CACAGGAGATGGTGACCAACCAACCCCTGATCAGATGATGAAACAGAGATGGTATTA 567  
Qy 623 GCCAGCACACCGCCAAAGGCCATGGAGCAGATGGCGGCGAGCAGCGAGCGCGAG 682  
Db 568 GCCAGTACCAACCGCTAAAGCCATGGAGCAGATGCGAGGGTTCGAGTGAGCAGGCGAGAG 627  
Qy 683 GCCATGAGGTGGCGAGCGCCAGCGAGCAGATGGTGAGGCCATGAGGACCATCGGCACC 742  
Db 628 GCCATGAGGTGCTGTAGTAAAGCTGAGCAGATGGTTCAGGCAATGAGAACCATTTGGGACC 687  
Qy 743 CACCCAGCAGCAGCGCGGCTGAAGAACGACCTGTGAGAACCTTGCAGGCGCTACCGAG 802  
Db 688 CACCTAGCTCCAGTGCGCGGTTTGAAGATGATCTCTTGAATAATTTGAGGCGCTACCGAG 747  
Qy 803 AAGCGCATGGCGGTGCAGATGCGAGCGCTTCAAGTGAAC 840  
Db 748 AAACGGATGGGAGTGCAAAATGCGAGGATTCAGAGTGATC 785

## RESULT 4

US-09-762-861B-1  
; Sequence 1, Application US/09762861B  
; Patent No. 6579528  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS (formerly HK2-033CPUS)  
; CURRENT APPLICATION NUMBER: US/09/762,861B  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION:  
; NAME/KEY: misc feature  
; LOCATION: (673)..(673)  
; OTHER INFORMATION: At nucleotide 673, r = a or g  
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val  
US-09-762-861B-1

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Query Match      56.6%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 76.8%; Pred. No. 3.6e-80;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

Qy 83 AGCCTGCTGACCGAGGTGGAGACTGCTGCTGAGCATCATCCCGAGCGCCCTCAAG 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28 AGTCTTCTGACCGAGGTGGAACGTACGTTCTCTATCGTACCATCAGGCCCCCTCAA 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 143 GCCGAGATCGCCAGAGCTGGAGAGCGTGTTCGCCGCGCAAGAACACCGACTCGAGGTG 202
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88 GCCGAGATCGCGAGAGACTTGAAGATGTCTTTCGAGGAAGAACACCGATCTTGAGGCA 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 203 CTGATGAGTGGCTGAAGACAGAGCCCATCTGTAGCCCTCTGACCAAGGGCATCTGGGC 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 148 CTCATGAAATGGCTTAAAGACAGACCAATCTCTGACCTCTGACTTAAAGGGATTTAGGA 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 263 TTCGTGTTCACTCCAGCGTCCCGAGGAGCGCGCTGACAGCGCCCGCTTCGTGCAG 322
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 208 TTCGTATTACGCTCACCGTCCAGTGAGCGAGACTGCGAGCGTACGCGCTTTGTCCAA 267
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 323 AACCCCTTGAACGGCAACGGCGACCCCAACCAACATGGAACAGGCGCGTGAAGCTGTACAGG 382
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 268 AATGCCCTTAGTGGAAACGGAGATTCATATGGGGCAAAAGAGGTGGCACTTATCCACT 327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 383 AAGCTGAAGAGGAGATCACCTTCACGCGCCCAAGGAGATCAGCCTGAGCTACAGGCC 442
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 328 AAGCTTAAAGAGAAATAACATTCATGGGGCAAAAGAGGTGGCACTTATCCACT 387
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 443 GCGCCCTGCGACGTGCTGAGCGCTGATCTACACAGGATGGCGCGGTGACACCGAG 502
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 GGTGCATGAGCACTGATGGGACTCATATACACAGAAATGGGAACTGTGACAAACGAA 447
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 503 GTGCGCTTGGCCCTGCTGCGCACCTTCCAGGGCGCAAGGAGATCAGCTTGAGCTACAGGCC 562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 448 GTGCAATTGGCTTGGTATGGCCACATGTGAACAGATCGTGTATCCAGCATCGATCT 507
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 563 CACAGGAGATGTTGACCAACCAACCCCTGTATCAGGACAGAGAACAGGATGGTGTG 622
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 508 CACAGGAGATGTTGACCAACCAACCCCTGTATCAGACATGAAACAGAAATGGTATTA 567
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 623 GCCAGCACCGCCAGGCGCATGGAGAGATGGCGGAGAGCGGCGGCGAGCGGCGAG 682
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 568 GCCAGTACCAGCGCTAAAGCCATGGAGCAGATGGCAGGGTTCGATGAGCAGGCGAGAG 627
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 683 GCCATGAGGTGGCGAGCGCCAGCAGATGGTGCAGGCGCATGAGGACCATCGGCACC 742
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 628 GCCATGAGGTGGCTAGTAAGCTAGGCTAGGAGATGGTTCAGGCAATGAGAACCATTTGGGACC 687
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 743 CACCCAGCAGCAGCGCGCTGAAAGAACACCTGTCTGGAGAACCTGCGAGGCGCTACAG 802
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 688 CACCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTCTGAAATTTTGCAGGCGCTACAG 747
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 803 AAGCGCATGGCGTGCAGATCGCGCTTCAAGTGAAC 840
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 748 AAACGGATGGGAGTGCAAAATGCAGCGATTCAAGTGATC 785
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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## RESULT 5

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US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
```

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; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1
```

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Query Match      56.6%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 76.8%; Pred. No. 3.6e-80;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

Qy 83 AGCCTGCTGACCGAGGTGGAGACTGCTGCTGAGCATCATCCCGAGCGCCCTCAAG 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28 AGTCTTCTGACCGAGGTGGAACGTACGTTCTCTATCGTACCATCAGGCCCCCTCAA 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 143 GCCGAGATCGCCAGAGGTGGAGAGCGTGTTCGCCGCGCAAGAACACCGACTCGAGGTG 202
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88 GCCGAGATCGCGAGAGACTTGAAGATGTCTTTCGAGGAAGAACACCGATCTTGAGGCA 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 203 CTGATGAGTGGCTGAAGACAGAGCCCATCTGTAGCCCTCTGACCAAGGGCATCTGGGC 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 148 CTCATGAAATGGCTTAAAGACAGACCAATCTCTGACCTCTGACTTAAAGGGATTTAGGA 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 263 TTCGTGTTCACTCCAGCGTCCCGAGGAGCGCGCTGACAGCGCCCGCTTCGTGCAG 322
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 208 TTCGTATTACGCTCACCGTCCAGTGAGCGAGACTGCGAGCGTACGCGCTTTGTCCAA 267
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 323 AACCCCTTGAACGGCAACGGCGACCCCAACCAACATGGAACAGGCGCGTGAAGCTGTACAGG 382
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 268 AATGCCCTTAGTGGAAACGGAGATTCATATGGGGCAAAAGAGGTGGCACTTATCCACT 327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGGGCGCAAGGAGATCAGCTTGAGCTACAGGCC 442
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 328 AAGCTTAAAGAGAAATAACATTCATGGGGCAAAAGAGGTGGCACTTATCCACT 387
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 443 GCGCCCTGCGACGTGCTGAGCGCTGATCTACACAGGATGGCGCGGTGACACCGAG 502
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 GGTGCATGAGCACTGATGGGACTCATATACACAGAAATGGGAACTGTGACAAACGAA 447
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 503 GTGCGCTTGGCCCTGCTGCGCACCTTCCAGGGCGCAAGGAGATCAGCTTGAGCTACAGGCC 562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 448 GTGCAATTGGCTTGGTATGGCCACATGTGAACAGATCGTGTATCCAGCATCGATCT 507
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 563 CACAGGAGATGTTGACCAACCAACCCCTGTATCAGGACAGAGAACAGGATGGTGTG 622
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 508 CACAGGAGATGTTGACCAACCAACCCCTGTATCAGACATGAAACAGAAATGGTATTA 567
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 623 GCCAGCACCGCCAGGCGCATGGAGAGATGGCGGAGAGCGGCGGCGAGCGGCGAG 682
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 568 GCCAGTACCAGCGCTAAAGCCATGGAGCAGATGGCAGGGTTCGATGAGCAGGCGAGAG 627
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 683 GCCATGAGGTGGCGAGCGCCAGCAGATGGTGCAGGCGCATGAGGACCATCGGCACC 742
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 628 GCCATGAGGTGGCTAGTAAGCTAGGCTAGGAGATGGTTCAGGCAATGAGAACCATTTGGGACC 687
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 743 CACCCAGCAGCAGCGCGCTGAAAGAACACCTGTCTGGAGAACCTGCGAGGCGCTACAG 802
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 688 CACCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTCTGAAATTTTGCAGGCGCTACAG 747
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 803 AAGCGCATGGCGTGCAGATCGCGCTTCAAGTGAAC 840
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 748 AAACGGATGGGAGTGCAAAATGCAGCGATTCAAGTGATC 785
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RESULT 6
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CI-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, xaa = Val
US-10-434-811A-1

Query Match      56.6%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 76.8%; Pred. No. 3.6e-80;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

Qy 83 AGCTGTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGAG 142
Db 28 AGTCTTCTGACCGAGGTGGAACGTACGTTCTCTATCATCATGACGAGCGGCCCTCAA 87
Qy 143 GCCGAGATCGCCAGAGCTGGAGGAGCTGTTGCGCGCAAGAACACCGAGCTGGAGTG 202
Db 88 GCCGAGATCGCGAGAGACTTGAAGATGTTCTTGCGGGAAGAACACCGATCTTGAGCA 147
Qy 203 CTGATGGAGTGGCTGAAGACCGAGGCCCATCTCTGAGCCCTTGACCAAGGGCATCTGGGC 262
Db 148 CTCATGGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAAAGGGATTTAGGA 207
Qy 263 TTCGTGTTACCTGACCGTGGCCAGCGAGCGGCCCTGAGCGCGCGCTTCGTGAG 322
Db 208 TTCTGTAATTCAGCTCACCGTGGCCAGTGGAGGACTGCGAGCGTACGCTTTGTCAA 267
Qy 323 AACGCCCTGAACGGCAACGGGACCCCAACACATGGACAAGCGGTGAAGCTGTACAGG 382
Db 268 AATGCCCTTAGTGGAAACGGAGATCCAAACACATGTGACAGACAGATTAAGCTGTACAGG 327
Qy 383 AAGCTTGAAGAGGAGATCACCTTCCACGGCGCCCAAGGAGATCAGCTGAGCTACAGCGCC 442
Db 328 AAGCTTAAAGAGAATAAATTCATTCATGGGCAAGAGGTGGCACTCAGCTATTCCACT 387
Qy 443 GCGCGCTTGGCCAGCTGATGGCCCTGATCTTAAACAGGATGGGCGCGGTGACACCGAG 502
Db 388 GGTGCACTAGCCAGCTGATGGGACTCATATACAGAAATGGGAACTGTGACAAACCGAA 447
Qy 503 GTGGCTTTCGCTGGTGGCCACCTGCGAGCAGATCGCGACAGCCAGCCAGCCGAGC 562
Db 448 GTGGCAATTTGGCTGGTATGGCCACATGTGAACAGATCGCTGATTCACGATCGATCT 507
Qy 563 CACAGCGAGATGGTGACCAACCAACCCCTGTATCAGGCAACGAGATGGTGCTG 622
Db 563 CACAGCGAGATGGTGACCAACCAACCCCTGTATCAGGCAACGAGATGGTGCTG 622

RESULT 7
US-09-311-784A-13
; Sequence 13, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
; OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
; OTHER INFORMATION: influenza matrix protein gene
; NAME/KEY: CDS
; LOCATION: (16)..(816)
; OTHER INFORMATION: PADRE-Influenza matrix
US-09-311-784A-13

Query Match      56.6%; Score 477.4; DB 3; Length 816;
Best Local Similarity 75.6%; Pred. No. 3.8e-80;
Matches 592; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

Qy 56 GCCTGTGCCCTGACCCAGACCTGGGCTAGCTCTGACCCAGGTGGAGACCTAGTCTG 115
Db 34 GCCTGGACCTCGAAGGCTGCGGCTATGAGTCTTTCTAACCGAGGTGCGAACGTACGTTCTC 93
Qy 116 AGCATCATCCCCAGCGGCCCTTGAAGCCGAGATCGCCAGAGGCTGGAGGAGCTGTTTC 175
Db 94 TCTATCATCCATCAGGCCCTTCAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTTT 153
Qy 176 GCGCGCAAGAACCCGACCTGGAGGTGCTGATGAGTGGCTGAAGACACGAGCCCATCTG 235
Db 154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCTG 213
Qy 236 AGCCCCCTGACCAAGGGCATCTCTGGGCTTGTGTTTCACTGACCGTGCCTCCAGCGAGCGC 295
Db 214 TCACCTCTGATAGGGNAATTTTAGGGTTTGTGTTTCACTGCTCACCGTGCCTCCAGTGAGCGA 273
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Qy 296 GGCCTGCAGCGCCGCTTCTGTCAGAACGCGCTGAAACGCGACGGGACCCCAAC 355  
Db 274 GGACTGCAGCGTAGACGATTGTCCAAATGCGCTTAAATGGGAATGGAGACCCCAAC 333  
Qy 356 ATGACAAAGGCGGTGAAGCTGTACAGGAAGCTGAAGAGGAGATCACTTCCACGGCGCC 415  
Db 334 ATGACAGGCGGATTAACATATACAGAGCTGAAGAGGGAATGACATTCATGGAGCA 393  
Qy 416 AAGGAGATGACCTGAGCTACAGCGCGCGCCCTTGGCCAGCTGCATGGGCTGATCTAC 475  
Db 394 AAGGAAGTTGCACTCAGTTACTCAACTGGTGGCTTGGCAGTTGCATGGGTCTCATATAC 453  
Qy 476 AACAGGATGGCGCGCTGACACCGAGGTGGCTTGGCCCTGGTGTGGGCCACCTGCGAG 535  
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Qy 776 CTGCTGGAGAACCTGCGAGCGCTTACAGAGCGCATGGGCGTGCAGATGCGAGCGCTTCAAG 835  
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Qy 836 TGA 838  
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## RESULT 8

US-09-506-286B-4  
; Sequence 4, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; PRIOR FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
US-09-506-286B-4  
Query Match 56.3%; Score 474.8; DB 3; Length 1023;  
Best Local Similarity 76.6%; Pred. No. 1.2e-79;  
Matches 581; Conservative 0; Mismatches 177; Indels 0; Gaps 0;  
Qy 83 AGCCTGCTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGGCGGCCCTGAG 142

Db 28 AGTCTTCTGACCGAGGTGAAACGTAAGTCTCTCTATCTTACCATCAGGCCCCCTCAAA 87  
Qy 143 GCCAGATGCCCGAGAGGTGGAGAGCTGTTCCGCGGCAAGAACACCGACCTGGAGGTG 202  
Db 88 GCCAGATGCCCGAGAGACTTGAAGATGTTTGCAGGGAAGAACACCGATCTTGAGGCA 147  
Qy 203 CTGATGAGTGGCTGAAGACCGAGGCGCCCTGAGCCCTGACCAAGGCGATCCTGGGC 262  
Db 148 CTCATGGAATGGCTAAAGACAAAGCAATCTCTGACTTGAACGGAATTTAGGA 207  
Qy 263 TTGCTGTTCACCTGACCGCGGCGGCTGCGAGCGCGGCTGCGAGCGCGGCTTCTGTCAG 322  
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Db 568 GCCAGTACACCGCTAAGCCATGGAGCAGATGGCAGGCTCGAGTGGAGGCGGCGGCGGCGG 627  
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US-09-762-861B-4  
; Sequence 4, Application US/09762861B  
; Patent No. 6579528  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)  
; CURRENT APPLICATION NUMBER: US/09/762,861B  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 1023









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Db 484 CACAGGAGATGGTACACCAACCAACCCCTGTATTCAGGACGAGAACAGGATGGTGTG 543  
Qy 623 GCCAGCACCGCCCAAGGCCATGAGAGAGATGGCCGCGCAGCAGCAGCAGCAGCAGCAG 682  
Db 544 GCCAGTACACCGCTAAAGCCATGAGCAGATGGCAGGCTCGAGTGACGAGCAGCAGAG 603  
Qy 683 GCCATGAGAGTGGCCAGCCAGGACGAGCAGATGGTGTGAGGACATGAGGACCATGGCACC 742  
Db 604 GCCATGAGAGTGGTGTGAGGAGCAGATGGTGTGAGGAGCAGATGGTGTGAGGAGC 663  
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## RESULT 13

US-09-762-861B-3  
; Sequence 3, Application US/09762861B  
; Patent No. 6579528  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; FILE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; CURRENT APPLICATION NUMBER: US/09/762,861B  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-09-762-861B-3

Query Match 56.2%; Score 474.2; DB 3; Length 756;  
Best Local Similarity 76.8%; Pred. No. 1.5e-79;  
Matches 578; Conservative 1; Mismatches 174; Indels 0; Gaps 0;  
Qy 83 AGCTGTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGGAAG 142  
Db 4 AGTCTTCTGACCGAGGTGGAACGTACGTCTCTCTATCGTACCATCAGGCCCTCAA 63  
Qy 143 GCCAGATGCGCCAGAGCTGGAGACGTGTTCGCCGGAAGAACACCGACCTGGAGTG 202  
Db 64 GCCAGATGCGCGAGACTTGAAGATGTCTTTGAGGGAAGAACACCGATCTTGAGGCA 123  
Qy 203 CTGATGAGTGGCTGAAGACCGCCCATCTGTAGCCCTTGAACAGGGCATCTCTGGGC 262  
Db 124 CTCATGGAATGGCTAAAGACAGACCAATCTCTGACCTCTGACCTAAGAGGATTTAGGA 183  
Qy 263 TTGCTGTTTCACTGACCGTGCACGAGCGCGCTGTGACGCGCGCGCTTGTGCGAG 322  
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Qy 383 AAGCTGAAGAGGGAGATCACCTTCCAGCGCCCAAGAGAGATCAGCTGTAGCTACAGCGCC 442  
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Qy 563 CACAGGAGATGGTGAACACCAACCCCTGTATTCAGGACGAGAACAGATGGTGTG 622  
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Db 604 GCCATGAGAGTGGTGTGAGGAGCAGATGGTGTGAGGAGCAGATGGTGTGAGGAGC 663  
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## RESULT 14

US-10-065-133A-3  
; Sequence 3, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-3

Query Match 56.2%; Score 474.2; DB 3; Length 756;  
Best Local Similarity 76.8%; Pred. No. 1.5e-79;  
Matches 578; Conservative 1; Mismatches 174; Indels 0; Gaps 0;  
Qy 83 AGCTGTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGGAAG 142  
Db 4 AGTCTTCTGACCGAGGTGGAACGTACGTCTCTCTATCGTACCATCAGGCCCTCAA 63  
Qy 143 GCCAGATGCGCCAGAGCTGGAGACGTGTTCGCCGGAAGAACACCGACCTGGAGTG 202  
Db 64 GCCAGATGCGCGAGACTTGAAGATGTCTTTGAGGGAAGAACACCGATCTTGAGGCA 123  
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US-10-434-811A-3
; Sequence 3, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-434-811A-3
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Query Match      56.2%; Score 474.2; DB 3; Length 756;
Best Local Similarity 76.8%; Pred. No. 1.5e-79;
Matches 578; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

Qy      83  AGCTGTCTGACCGAGGTGGAGACCTTACGTGTGTGAGCATCATCCCCAGCGGCCCTGAAG 142
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Qy      503  GTGGCCCTTGGCCCTGGTGGCGCACCTGCGAGCAGATCGCCGACAGCAGCAGCCGAGC 562
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GenCore version 5.1.7  
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| 4          | 762   | 90.3          | 942    | 8     | US-10-729-830-6  |
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| 6          | 485.8 | 57.7          | 942    | 8     | US-10-729-830-5  |
| 7          | 485.8 | 57.6          | 774    | 8     | US-10-729-830-1  |
| 8          | 481.2 | 57.0          | 1027   | 8     | US-10-177-390-31 |
| 9          | 478   | 56.6          | 1027   | 8     | US-10-855-875-5  |
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| 35 | 80    | 9.5  | 1332 | 6 | US-10-375-932-318  | Sequence 318, App  |
| 36 | 80    | 9.5  | 1380 | 6 | US-10-375-932-189  | Sequence 189, App  |
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| 38 | 78.8  | 9.3  | 1092 | 6 | US-10-138-098-13   | Sequence 13, Appli |
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| 40 | 78.8  | 9.3  | 3020 | 6 | US-10-138-098-21   | Sequence 21, Appli |
| 41 | 78.8  | 9.3  | 3020 | 8 | US-10-476-615-21   | Sequence 21, Appli |
| 42 | 78.8  | 9.3  | 3021 | 6 | US-10-138-098-22   | Sequence 22, Appli |
| 43 | 78.8  | 9.3  | 3021 | 6 | US-10-138-098-23   | Sequence 23, Appli |
| 44 | 78.8  | 9.3  | 3021 | 6 | US-10-138-098-24   | Sequence 24, Appli |
| 45 | 78.8  | 9.3  | 3021 | 8 | US-10-476-615-22   | Sequence 22, Appli |

ALIGNMENTS

RESULT 1  
US-10-729-830-4  
; Sequence 4, Application US/10729830  
; Publication No. US20050032730A1  
; GENERAL INFORMATION:  
; APPLICANT: Von der Muelbe, Florian  
; APPLICANT: Hoerr, Ingmar  
; APPLICANT: Pasciolo, Steve  
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA  
; FILE REFERENCE: 2793-1-001PCT/CIP  
; CURRENT APPLICATION NUMBER: US/10/729,830  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: PCT/EP02/06180  
; PRIOR FILING DATE: 2002-06-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 844  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Influenza  
; OTHER INFORMATION: matrix: gene for secreted form (with N-terminal  
; OTHER INFORMATION: signal sequence) with increased G/C-content  
; FEATURE:  
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop  
; OTHER INFORMATION: codon: tga (nucleotides 836 to 838)  
US-10-729-830-4

|                       |                 |  |           |             |
|-----------------------|-----------------|--|-----------|-------------|
| Query Match           | 100.0%;         | Score 844;   | DB 8;     | Length 844; |
| Best Local Similarity | 100.0%;         | Pred. No. 7.6e-190;  |           |             |
| Matches 844;          | Conservative 0; | Mismatches 0;  | Indels 0; | Gaps 0;     |
| Qy                    | 1               | AGATCTAAAGATGCGCTCATGGCCCCCGCACCCCTGGTGTGCTGTGCTGCTGAGCGGCGCCT | 60        |             |
| Db                    | 1               | AGATCTAAAGATGCGCTCATGGCCCCCGCACCCCTGGTGTGCTGTGCTGAGCGGCGCCT    | 60        |             |
| Qy                    | 61              | GGCCCTGACCCAGACCTGGGCTAGCCTGTGCTGACCGAGGTGGAGACCTACGTTCTGAGCAT | 120       |             |
| Db                    | 61              | GGCCCTGACCCAGACCTGGGCTAGCCTGTGCTGACCGAGGTGGAGACCTACGTTCTGAGCAT | 120       |             |
| Qy                    | 121             | CATCCCCAGCGGCCCTCTGAAGCGCCGAGATCGCCAGAGGTGGAGACCTGTTTCGCGCG    | 180       |             |
| Db                    | 121             | CATCCCCAGCGGCCCTCTGAAGCGCCGAGATCGCCAGAGGTGGAGACCTGTTTCGCGCG    | 180       |             |



; Sequence 3, Application US/10729830  
; Publication No. US20050032730A1  
; GENERAL INFORMATION:  
; APPLICANT: Von der Muelbe, Florian  
; APPLICANT: Hoerr, Ingrid  
; APPLICANT: Pascalo, Steve  
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA  
; FILE OF INVENTION: Optimised for translation in its coding regions  
; FILE REFERENCE: 2793-1-001PCT/CIP  
; CURRENT APPLICATION NUMBER: US/10/729,830  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: PCT/EP02/06180  
; PRIOR FILING DATE: 2002-06-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 775  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Influenza  
; OTHER INFORMATION: matrix: gene with increased G/C-content  
; FEATURE:  
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop  
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)  
US-10-729-830-3

Query Match 90.3%; Score 762; DB 8; Length 775;  
Best Local Similarity 100.0%; Pred. No. 1.8e-170;  
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 83 AGCTGTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGAAG 142  
Db 14 AGCTGTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGAAG 73  
Qy 143 GCCGAGATGCCCCAGAGCTGGAGAGCGTGTTCGCCGCAAGAACACCGACCTGGAGTG 202  
Db 74 GCCGAGATGCCCCAGAGCTGGAGAGCGTGTTCGCCGCAAGAACACCGACCTGGAGTG 133  
Qy 203 CTGATGGAGTGGCTGAGACAGCGCCCATCTGTAGCCCTTGTGACAGGAGGATCTCTGGC 262  
Db 134 CTGATGGAGTGGCTGAGACAGCGCCCATCTGTAGCCCTTGTGACAGGAGGATCTCTGGC 193  
Qy 263 TTCGTGTTACCTGACCGTGCAGCGAGCGCGCTGTGACAGCGCGCTGTGAGCGCGCTTGTGAG 322  
Db 194 TTCGTGTTACCTGACCGTGCAGCGAGCGCGCTGTGACAGCGCGCTGTGAGCGCGCTTGTGAG 253  
Qy 323 AACGCCCTGAACGGCAACGGCGACCCCAACCAATGGAACAGGCGCGTGAAGCTGTACAGG 382  
Db 254 AACGCCCTGAACGGCAACGGCGACCCCAACCAATGGAACAGGCGCGTGAAGCTGTACAGG 313  
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGGAGATGATGAGCTGACAGCGCC 442  
Db 314 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGGAGATGATGAGCTGACAGCGCC 373  
Qy 443 GCGCCCTTGGCCAGCTGATGGGCTGATCTACAAACAGAGTGGCGCGCTGACCAACCGAG 502  
Db 374 GCGCCCTTGGCCAGCTGATGGGCTGATCTACAAACAGAGTGGCGCGCTGACCAACCGAG 433  
Qy 503 GTGGCCCTTGGCCCTGGTGTGGCCACCTGCGAGCAGATTCGCCGACAGCACCGCAGC 562  
Db 434 GTGGCCCTTGGCCCTGGTGTGGCCACCTGCGAGCAGATTCGCCGACAGCACCGCAGC 493  
Qy 563 CACAGGCGAGTGGTGAACACACCAACCCCTGTATGAGGACGAGAACAGGATGGTGTG 622  
Db 494 CACAGGCGAGTGGTGAACACACCAACCCCTGTATGAGGACGAGAACAGGATGGTGTG 553  
Qy 623 GCCAGCACCGCCAGAGGCGATGAGCAGATGGCCGCGAGCAGCAGCGCGCGCGAG 682  
Db 554 GCCAGCACCGCCAGAGGCGATGAGCAGATGGCCGCGAGCAGCAGCGCGCGCGAG 613  
Qy 683 GCCATGGAGTGGCCAGCGAGCGCGAGGAGATGGTGTGAGGCGCATGAGGACCATCGGCACC 742  
Db 742

Db 614 GCCATGGAGTGGCCAGCGAGCGCGAGCGAGATGGTGTGAGGACCATGAGGACCATCGGCACC 673  
Qy 743 CACCCAGCAGCAGCGCGCGCTGAAGAACAGCAGCTGTGGAGAACCTGCGAGGCTTACCAG 802  
Db 674 CACCCAGCAGCAGCGCGCGCTGAAGAACAGCAGCTGTGGAGAACCTGCGAGGCTTACCAG 733  
Qy 803 AAGCGCATGGCGTGCAGATGACGCGCTTCAAGTGAATAGT 844  
Db 734 AAGCGCATGGCGTGCAGATGACGCGCTTCAAGTGAATAGT 775

RESULT 4  
US-10-729-830-6  
; Sequence 6, Application US/10729830  
; Publication No. US20050032730A1  
; GENERAL INFORMATION:  
; APPLICANT: Von der Muelbe, Florian  
; APPLICANT: Hoerr, Ingrid  
; APPLICANT: Pascalo, Steve  
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA  
; FILE OF INVENTION: Optimised for translation in its coding regions  
; FILE REFERENCE: 2793-1-001PCT/CIP  
; CURRENT APPLICATION NUMBER: US/10/729,830  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: PCT/EP02/06180  
; PRIOR FILING DATE: 2002-06-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 942  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Influenza  
; OTHER INFORMATION: matrix: mRNA with increased G/C-content and  
; OTHER INFORMATION: stabilisation sequences  
; FEATURE:  
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-  
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,  
; OTHER INFORMATION: respectively.  
; FEATURE:  
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop  
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)  
US-10-729-830-6

Query Match 90.3%; Score 762; DB 8; Length 942;  
Best Local Similarity 87.9%; Pred. No. 1.8e-170;  
Matches 670; Conservative 92; Mismatches 0; Indels 0; Gaps 0;  
Qy 83 AGCTGTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGAAG 142  
Db 59 AGCCUGUGUACCGAGGUGGAGACCUACGUGUGAGCAUCCUCCAGCGGCCCGCCUGAAG 118  
Qy 143 GCCGAGATGCCCGAGGCTGGAGAGCGTGTTCGCCGCAAGAACACCGACCTGGAGTG 202  
Db 119 GCCGAGATGCCCGAGGCTGGAGAGCGTGTTCGCCGCAAGAACACCGACCTGGAGTG 178  
Qy 203 CTGATGAGTGGCTGAAGACAGCGCCCATCTGTAGCCCTTGTGACAGGAGGATCTCTGGC 262  
Db 179 CUGAUGGAGUGGUGAAGACAGCAGGCCCAUCCUGAGCCCGCCUCCAGGAGGAGGAG 238  
Qy 263 TTCGTGTTACCTGACCGTGCAGCGCGCGCTGTGAGCGCGCTGAGCGCGCTGTGTCAG 322  
Db 239 UUCGUGUUCUACCGUCCG 298  
Qy 323 AACGCCCTGAACGGCAACGGCGACCCCAACCAATGGAACAGGCGCGTGAAGCTGTACAGG 382  
Db 299 AACGCCCTGAACGGCAACGGCGACCCCAACCAATGGAACAGGCGCGGUGAAGGAGG 358  
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGGAGATGAGCTGAGCTACAGGCC 442  
Db 359 AAGCTGAAGAGGAGGAGATCACCTTCCAGCGCGCCCAAGGAGGAGGAGGAGGAGGAG 418









;  
; TITLE OF INVENTION: Polynucleotides by Electroporation  
; FILE REFERENCE: 021505wo/JH/ml  
; CURRENT APPLICATION NUMBER: US/10/177,390  
; CURRENT FILING DATE: 2002-06-20  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: Influenza virus  
US-10-177-390-31

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Query Match      57.0%; Score 481.2; DB 6; Length 1027;
Best Local Similarity 77.2; Pred. No. 3.9e-104;
Matches 585; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

Qy 83 AGCTGTGTGACCGAGGTGGAGACTTACGTGCTGAGACATCATCCCGAGCGGCCCTCTGAAG 142
Db 29 AGTCTTCTAACCGAGGTGGAACGTAAGTCTCTCTATCATCCCGTCAGGCCCTCTCAA 88

Qy 143 GCCGAGATCGCCAGAGGCTGGAGACGTGTTCGCCGCAAGAACACCGACCTGGAGGTG 202
Db 89 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGACGGGAAGAACCCGATCTTGAGGTT 148

Qy 203 CTGATGAGTGGCTGAAGACACAGGCCCATCTCTGAGCCCCCTGACCAAGGGCATCTCGGC 262
Db 149 CTCATGGAATGGCTAAGACAAAGACCAATCTCTGACCTCTGACTAAGGGGATTTTAGGA 208

Qy 263 TTGCTGTTCACCTGACCGTCCCGACGAGCGCGCTGACGCGCCCGCTTCGTGCAG 322
Db 209 TTTGTGTTCAGCTCACCGTCCCGACGTGAGCGAGACTGACGCGTGTGTCAG 268

Qy 323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGAACAGGCGCTGAAGCTGTACAGG 382
Db 269 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAGCAGTTAAACTGTATAGG 328

Qy 383 AAGCTGAAGAGGAGATCACCTTTCACGCGGCTGATCTACACAGGATGGCGCGTACACCGAG 502
Db 389 GGTGCACCTTGCCAGTTGTATGGGCTCTATATACACAGGATGGGGCTGTGACCACTGAA 448

Qy 503 GTGGCTTTGGCCTGGTATGTGCAACCTGTGAA CAGATTGCTGACTCCACGATCGGTCT 508
Db 449 GTGGCAATTTGGCCTGGTATGTGCAACCTGTGAA CAGATTGCTGACTCCACGATCGGTCT 508

Qy 563 CACAGGCAGATGGTGACACCAACCAACCCCTGATCAGGCACGAGACAGGATGGTGTG 622
Db 509 CATAGGCAAAATGGTGACACCAACCAACCCCTGATCAGGCACGAGACAGGATGGTGTG 568

Qy 623 GCCAGCACACCGCCAGGCCATGGAGCAGATGGCCCGGACGATGAGACAGAGATGGTTTA 682
Db 569 GCCAGCACATAGCTAAGGCTATGGAGCAATGGCTGATCAGATGAGACAGAGATGGTTTA 682

Qy 683 GCCATGAGGTGGCCAGCAGGCCAGGAGAGATGGTGACAGGCGCATGAGGACCATCGGCACC 742
Db 629 GCCATGAGGTGGCTAGTCAGGCTAGGCAATGGTGCAAGCGATGAGAACCATTTGGGACT 688

Qy 743 CACCCACGACGAGCGCGGCTGAGAACACCTCTGAGAGACCTTGAGGACCTTACCG 802
Db 689 CATCTAGCTCCAGTGTGGTCTGAAAAAATGATCTCTTTGAAAAATTTGAGGCTATCAG 748

Qy 803 AAGCGCATGGCGGTGCAGATCAGCGCTTCAAGTGAAC 840
Db 749 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786
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RESULT 9  
US-10-855-875-5  
; Sequence 5, Application US/10855875  
; Publication No. US2005003349A1

;  
; GENERAL INFORMATION:  
; APPLICANT: Kawaoka, Yoshihiro  
; TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene  
; FILE REFERENCE: 800.038US1  
; CURRENT APPLICATION NUMBER: US/10/855,875  
; CURRENT FILING DATE: 2004-05-27  
; PRIOR APPLICATION NUMBER: US 60/473,798  
; PRIOR FILING DATE: 2003-05-28  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: Influenza virus  
US-10-855-875-5

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Query Match      56.6%; Score 478; DB 8; Length 1027;
Best Local Similarity 76.9%; Pred. No. 2.2e-103;
Matches 583; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

Qy 83 AGCTGTGTGACCGAGGTGGAGACCTTACGTGCTGAGCATCATCCCGAGCGGCCCTCTGAAG 142
Db 29 AGTCTTCTAACCGAGGTGGAACGTAAGTCTCTCTATCATCCCGTCAGGCCCTCTCAA 88

Qy 143 GCCGAGATCGCCAGAGGCTGGAGAGCTGTTCGCCGCAAGAACACCGACCTGGAGGTG 202
Db 89 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGACGGGAAGAACACCGATCTTGAGGTT 148

Qy 203 CTGATGAGTGGCTGAAGACACAGGCCCATCTCTGAGCCCCCTGACCAAGGGCATCTCTGGC 262
Db 149 CTCATGGAATGGCTAAGACAAAGACCAATCTCTGACCTCTGACTAAGGGGATTTTAGGA 208

Qy 263 TTGCTGTTCACCTGACCGTCCCGACGAGCGCGCTGACGCGCCCGCTTCGTGCAG 322
Db 209 TTTGTGTTCAGCTCACCGTCCCGACGTGAGCGAGGACTGACGCGTGTGACACTTTGTCAA 268

Qy 323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGAACAGGCGCTGAAGCTGTACAGG 382
Db 269 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAGCAGTTAAACTGTATAGG 328

Qy 383 AAGCTGAAGAGGAGATCACCTTTCACGCGCGCCCAAGGAGATCAGCTGTAGCTACAGCGCC 442
Db 329 AAGCTCAAGAGGAGATTAACATTTCCATGGGGCCCAAGAAATCTCACTCAGTTATCTGCT 388

Qy 443 GGGCCCTGCGCAGCTGATGGGCTGTATCTCAACAGGATGGGCGCGTGAACCCAG 502
Db 389 GGTGCACCTTGCCAGTTGTATGGGCTCTATATACCAACAGGATGGGGCTGTGACCACTGAA 448

Qy 503 GTGGCTTTGGCCTGGTGTGCGCACCTGCGAGCAGATCCCGACAGCCAGCAGCGCAGC 562
Db 449 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAA CAGATTGCTGACTCCAGCATCGGTCT 508

Qy 563 CACAGGCAGATGGTGACACCAACCCCTGATCAGGCACGAGAACAGGATGGTGTG 622
Db 509 CATAGGCAAAATGGTGACACCAACCAACCCCTGATCAGGCACAGATGAGAACAGGATGGTTTA 568

Qy 623 GCCAGCACACCGCCAGGCCATGGAGCAGATGGCCCGGACGATGAGCAGGAGCGGCCGAG 682
Db 569 GCCAGCACATAGCTAAGGCTATGGAGCAATGGCTGATCAGATGAGACAGAGATGGTTTA 682

Qy 683 GCCATGAGGTGGCCAGCAGGCCAGGAGAGATGGTGACAGGCGCATGAGGACCATCGGCACC 742
Db 629 GCCATGAGGTGGCTAGTCAGGCTAGGCAATGGTGCAAGCGATGAGAACCATTTGGGACT 688

Qy 743 CACCCACGACGAGCGCGGCTGAGAACACCTCTGAGAGACCTTGAGGACCTTACCG 802
Db 689 CATCTAGCTCCAGTGTGGTCTGAAAAAATGATCTCTTTGAAAAATTTGAGGCTATCAG 748

Qy 803 AAGCGCATGGCGGTGCAGATGCAACGGCTTCAAGTGAAC 840
Db 749 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786
```

## RESULT 10

US-10-065-133A-1  
; Sequence 1, Application US/10065133A  
; Publication No. US20030199074A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (673)..(673)  
; OTHER INFORMATION: At nucleotide 673, r = a or g  
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val  
US-10-065-133A-1

Query Match 56.6%; Score 477.6; DB 6; Length 1023;  
Best Local Similarity 76.8%; Pred. No. 2.8e-103;  
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 83  | AGCCTGCTGACCGAGGTGGAGACCTACGCTGTGAGCATCATCCCGAGCGGCCCTCTGAAG  | 142 |
| Db | 28  | AGTCTTCTGACCGAGGTGGAACGTAAGTCTCTCTATCGTACCATCAGGCCCTCAA       | 87  |
| Qy | 143 | GCCGAGATGCGCCAGAGCTGGAGAGCGTGTTCGCGCCGCAAGAACACCGACTGGAGTG    | 202 |
| Db | 88  | GCCGAGATGCGCGAGAGCTTGAAGATGCTTTGCGAGGAAGAACACCGATCTTGAGCA     | 147 |
| Qy | 203 | CTGATGAGTGGCTGACACGAGCGCCATCTGAGCGCCCTGACCGCCCTGACCGGATCCTGGC | 262 |
| Db | 148 | CTCATGGAATGGCTTAAAGACCAAGACCAATCTCTGACTTGAAGGATTTAGGA         | 207 |
| Qy | 263 | TTCTGTTTACCCCTGACCGTGGCCGAGCGCGGCTGCGAGCGCCGCTTCTGTCAG        | 322 |
| Db | 208 | TTCTGTTTACCCCTGACCGTGGCCGAGCGCGGCTGCGAGCGCCGCTTCTGTCAG        | 267 |
| Qy | 323 | AACGCCCTTGAACGCGGACCGCCCAACCAATGGAACAGGCGGTGAAGCTGTACAGG      | 382 |
| Db | 268 | AATGCCCTTAGTGGAAACGAGATCCAAACCAACATGGAACAGGACAGTAAACCTGTACAGG | 327 |
| Qy | 383 | AAGCTGAGAGGAGATCACCTTCCAGCGCCGAGGAGATCAGCTGAGTACAGCGCC        | 442 |
| Db | 328 | AAGCTTAAAGAGAAATTAACATTTCCATGGGCAAAAGAGGTGGCACTCAGCTATTTCCACT | 387 |
| Qy | 443 | GGCGCCCTGGCCAGCTGATGAGGCTGATCTTACACAGAGTGGCGCGCTGACACCGAG     | 502 |
| Db | 388 | GGTGACCTAGCCAGCTGATGGGACTCATATACACAGANTGGGAACTGTGACACCGAA     | 447 |
| Qy | 503 | GTGGCTTTCGCGCTGTGCGCCACCTTCGAGCAGATTCGCGCAGCAGCAGCAGCGCAGC    | 562 |
| Db | 448 | GTGGCATTTGGCTTGGTATGCGCACATGTGAACAGATCGCTGATTTCCAGCATCGATCT   | 507 |
| Qy | 563 | CACAGGAGATGTTGAC    | 622 |
| Db | 508 | CACAGGAGATGTTGAC    | 567 |
| Qy | 623 | GCCAGCACCGCCCAAGGCCATGAGGAGCAGATGGCGCGCAGCAGCAGCGCGCGCGAG     | 682 |

|    |     |   |     |
|----|-----|---|-----|
| Db | 568 | GCCAGTACCACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGACGAG   | 627 |
| Qy | 683 | GCCATGAGGTGGCCAGCGCCAGCAGTGGTGAGGCCCATGAGGACCATCGGCACC      | 742 |
| Db | 628 | GCCATGAGGTGCTAGTAAGGCTTAGGCAGATGGTRCAGGCAATGAGAACCATTGGGACC | 687 |
| Qy | 743 | CACCCAGCAGCAGCGCGCCCTGAAGAACGACCTGCTGGAGAACCTGCGAGGCTTACGAG | 802 |
| Db | 688 | CACCTAGCTCCAGTGCGGGTTTGAAGATGATCTCTTGAANAATTTGCAGGCGCTACGAG | 747 |
| Qy | 803 | AAGCGCATGGCGTGCGAGATGCGCGCTTCAAGTGAAC                       | 840 |
| Db | 748 | AAACGATGGAGTGCAATATGACGATTTCAAGTGATC                        | 785 |

## RESULT 11

US-10-434-811A-1  
; Sequence 1, Application US/10434811A  
; Publication No. US20040022809A1  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS-1  
; CURRENT APPLICATION NUMBER: US/10/434,811A  
; CURRENT FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (663)..(663)  
; OTHER INFORMATION: At nucleotide 663, r = a or g  
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val  
US-10-434-811A-1

Query Match 56.6%; Score 477.6; DB 7; Length 1023;  
Best Local Similarity 76.8%; Pred. No. 2.8e-103;  
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 83  | AGCCTGCTGACCGAGGTGGAGACCTACGCTGTGAGCATCATCCCGAGCGGCCCTCTGAAG  | 142 |
| Db | 28  | AGTCTTCTGACCGAGGTGGAACGTAAGTCTCTCTATCGTACCATCAGGCCCTCAA       | 87  |
| Qy | 143 | GCCGAGATGCGCCAGAGCTGGAGAGCGTGTTCGCGCGCAAGAACACCGACTGGAGTG     | 202 |
| Db | 88  | GCCGAGATGCGCGAGAGCTTGAAGATGCTTTGCGAGGAAGAACACCGATCTTGAGGCA    | 147 |
| Qy | 203 | CTGATGAGTGGCTGAGACGAGCGCCATCTGAGCGCCCTGACCGCCCTGACCGGATCCTGGC | 262 |
| Db | 148 | CTCATGGAATGGCTTAAAGACCAAGACCAATCTCTGACTTGAAGGATTTAGGA         | 207 |
| Qy | 263 | TTCTGTTTACCCCTGACCGTGGCCGAGCGCGGCTGCGAGCGCCGCTTCTGTCAG        | 322 |
| Db | 208 | TTCTGTTTACCCCTGACCGTGGCCGAGCGCGGCTGCGAGCGCCGCTTCTGTCAG        | 267 |
| Qy | 323 | AACGCCCTTGAACGCGGACCGCCCAACCAATGGAACAGGCGGTGAAGCTGTACAGG      | 382 |
| Db | 268 | AATGCCCTTAGTGGAAACGAGATCCAAACCAACATGGAACAGGACAGTAAACCTGTACAGG | 327 |

Qy 383 AAGCTGAAGAGGAGATCACTTCCACGGGCGCCAAAGAGATCAACCTTGAGCTACAGCGCC 442  
Db 328 AAGCTTAAAGAGAAATAAATTCATCGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387  
Qy 443 GGCGCCCTGGCCAGCTGCATGGGCTGATCTACACAGGATGGCGCGGTGACCAACGAG 502  
Db 388 GGTGCATAGCCAGCTGCATGGGACTCATATACACAGATGGGAACTGTGACAAACGAA 447  
Qy 503 GTGGCCCTTGGCCCTGGTGGCCACCTGCGAGCAGATCGCCGACAGCCAGCAGCCGAGC 562  
Db 448 GTGGCATTTGGCCCTGGTATGGCCACATGTGAACAGATCGTGATTTCCAGCATCGATCT 507  
Qy 563 CACAGGAGATGGTGACACACCAACCCCTGTATCAGGACGACGAGAAACAGATGGTGTG 622  
Db 508 CACAGGAGATGGTGACAAACCAACCAACCCATTATACAGATGAAACAGAAATGGTATTA 567  
Qy 623 GCCAGCACCCGCAAGGCCATGGAGCAGATGGCGGACGAGCAGGAGCGCCGCGAG 682  
Db 568 GCCAGTACCAAGCGCTAAAGCCATGGAGCAGATGGCAGGGTTCGATGAGCAGGCGAGAG 627  
Qy 683 GCCATGAGGTGGCGAGCCAGCGCAGGAGATGGTGAGGCGCATGAGGACCATCGGCACC 742  
Db 628 GCCATGAGGTGTGTAGTAGGCTAGGACGAGATGGTGAGGCAATGAGAACCATTTGGNCC 687  
Qy 743 CACCCAGCAGCAGCGCGGCTGAAAGAACGACCTGTGGAGAACCTGCGAGGCGCTACAG 802  
Db 688 CACCCTAGCTCAGTGGCGGTTTGAAGATGATCTCTCTTGAATAATTTGCAGGCGCTACAG 747  
Qy 803 AAGCGCATGGCGTGCAGATCAGCGCTTCAAGTGAAC 840  
Db 748 AAACGGATGGGAGTGCAAAATCGACGATTTCAAGTGATC 785

## RESULT 12

US-10-734-373-1

; Sequence 1, Application US/10734373  
; Publication No. US20040137015A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/734,373  
; CURRENT FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (673)..(673)  
; OTHER INFORMATION: At nucleotide 673, r = a or g  
; OTHER INFORMATION: At amino acid residue 213, xaa = Val  
US-10-734-373-1

Query Match 56.6%; Score 477.6; DB 7; Length 1023;

Best Local Similarity 76.8%; Pred. No. 2.8e-103;

Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

Qy 83 AGCTGTGACCGAGGTGAGACCTACGTGTGAGCATATCCCGAGCGGCCCTGAGG 142

Db 28 AGTCTTGTGACCGAGGTGGAACGTACGTTCCTCTAATCGTACCATCATGAGCGGCCCTCAAA 87

Qy 143 GCCAGATGCCAGAGGCTGAGGAGCTGTTCCCGGCGACAGAACACCCGACCTGGAGGTG 202  
Db 88 GCCAGATCGCGAGAGACTTGAAGATGTCTTTTCAGGGGAAGAACACCCGATCTTGAGGCA 147  
Qy 203 CTCATGAGTGGCTGAAGACAGCGCCCATCTCAGAGCCCTGACCAAGGGGATCTCTGGGC 262  
Db 148 CTATGGAATGGCTTAAAGACAGACCAATCTCTACCTCTGACTTAAAGGATTTAGGA 207  
Qy 263 TTCTGTGTTCAACCTTACCGTCCAGCGAGCGCGGCTGCAGCGCCCGCCCTTCGTGTCAG 322  
Db 208 TTCTGTTATTCAGCTCACCGTGGCCAGTGAAGCGGAGTGCAGCGTAGACGCTTTGTCAA 267  
Qy 323 AAGCCCTTGAACGGCAACGGCGACCCCAACATGACAGAGCCGCTGAAGCTGTACAGG 382  
Db 268 AATGCCCTTATAGTGGAAACGGAGATCCAAACAACTGACAGACAGTAAACCTGTACAGG 327  
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGGCGCAAGAGATCAGCCTGAGCTACAGCGCC 442  
Db 328 AAGCTTAAAGAGAAATAACATTTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387  
Qy 443 GGCGCCCTGGCCAGCTGTCATGGGCTGATCTCAACAGAGATGGCGCGCTGACCAACGAG 502  
Db 388 GGTGCATAGCCAGCTGCATGGGACTCATATACACAGATGGGAACTGTGACAAACGAA 447  
Qy 503 GTGGCCCTTGGCCCTGGTGGCCACCTGCGAGCAGATCGCCGACAGCAGCAGCCGAGC 562  
Db 448 GTGGCATTTGGCCCTGGTATGCGCCACATGTGAAACAGATCGCTGATTTCCAGCATCGATCT 507  
Qy 563 CACAGGAGATGGTGACCAACCAACCCCTCATCAGGACGAGACGAGAACAGATGGTGTCTG 622  
Db 508 CACAGGAGATGGTGACAAACCAACCCCTTAATCAGACTGAAACAGAAATGGTATTA 567  
Qy 623 GCCAGCACCAACCGCCAGGCGCATGAGCAGATGGCGGACAGCAGCAGCGCGCGAG 682  
Db 568 GCCAGTACCAAGCGCTAAAGCCATGGAGCAGATGGCAGGGTTCGATGAGCAGGCGAGAG 627  
Qy 683 GCCATGAGGTGGCGAGCGCAGGCGCAGGAGATGGTGAGGCGCATGAGGACCATCGGCACC 742  
Db 628 GCCATGAGGTGTCTAGTAGGCTTAGCAGATGGTTCAGGCAATGAGAACCATTTGGGACC 687  
Qy 743 CACCCAGCAGCAGCGCGGCTGAAAGACGACCTGTGGAGAACCTGCGAGGCGCTACAG 802  
Db 688 CACCCTAGCTCAGTGGCGGTTTGAAGATGATCTCTTGAATAATTTGCAGGCGCTACAG 747  
Qy 803 AAGCGCATGGCGTGCAGATGAGCGCTTCAAGTGAAC 840  
Db 748 AAACGGATGGGAGTGCAAAATGCAGCGATTTCAAGTGATC 785

## RESULT 13

US-10-872-014-1

; Sequence 1, Application US/10872014  
; Publication No. US20040234553A1  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS-1  
; CURRENT APPLICATION NUMBER: US/10/872,014  
; CURRENT FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/434,811  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: 09/762,861  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1

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/ LENGTH: 1023
/ TYPE: DNA
/ ORGANISM: Equine influenza virus H3N8
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (25)..(780)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (663)..(663)
/ OTHER INFORMATION: At nucleotide 663, r = a or g
/ OTHER INFORMATION: At amino acid residue 213, xaa = Val
US-10-872-014-1

Query Match      56.6%; Score 477.6; DB 8; Length 1023;
Best Local Similarity 76.8%; Pred. No. 2.8e-103;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

QY 83 AGCTGTGTCACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCAGCGGCCCTCTGAAG 142
Db 28 AGTCTTCTGACCGAGTGGAAAGTACGTTCCTCTATCGTACCATCAGGCCCTCTCAA 87

QY 143 GCCGAGATGCCCGACGAGCTGGAGACGTGTTGCGCGGCAAGAACACCGACCTGAGGTG 202
Db 88 GCCGAGATGCCCGACGAGACTTGAAGATGTCTTTGCGAGGGAAGAACACCGATCTTGAGCA 147

QY 203 CTGATGGAGTGGCTGAAGACGAGGCCCATCTGTAGCCCTCTGACCAAGGGCATCTGGGC 262
Db 148 CTCATGGAAATGGCTAAGACAAAGCAATCTGTCACTCTGTACTAAGAGGATTTTGA 207

QY 263 TTGCTGTTTCACTTACCTGACCGTCCAGCGAGCGCGCTGTGACGCGCGCTTGTGCGAG 322
Db 208 TTGCTGTTTCACTTACCTGACCGTCCAGTGGAGGAGTGTGACGCTTTGTCCAA 267

QY 323 AACGCCCTGAACGGCAACGGGACCCCAACATGGAACAGGCGGTGAAGCTGTACAGG 382
Db 268 AATGCCCTTAGTGGAAACGGAGATCCAAACAACTGGAAGAGAGTAAAACTGTACAGG 327

QY 383 AAGCTGAAGAGGAGATCACCTTCCACGCGCCGAAGGAGATCAGCTGAGCTACAGGCC 442
Db 328 AAGCTTAAAGAGAAATTAACATTCATGGGGCAAGAGGTGGCACTCAGCTATTCCACT 387

QY 443 GCGCCCTTGGCAGCTGATGGGCTGTATCTAACACAGGATGGGCGCGTGACCAACCGAG 502
Db 388 GTGCACTAGCCAGCTGATGGGATCTCATATACACAGATGGGAACTGTGCAACCGAA 447

QY 503 GTGGCTTTGGCCTGTGTGCGCCACTGTGCGAGCAGATGCGCGACAGCCAGACCGCAGC 562
Db 448 GTGGCATTTGGCCTGGTATGGGCCACATGTGAACAGATCGCTGATTTCCAGCATCGATCT 507

QY 563 CACAGGCAGATGGTGACCAACCAACCCCTGTATCAGGCACGAGACAGGATGGTGTG 622
Db 508 CACAGGCAGATGGTGACCAACCAACCCCTTAATCAGACATGAACACAGAAATGGTATTA 567

QY 623 GCCACACACCGCCCAAGGCCATGGAGCAGATGGCGCGCAGCAGCAGCGCGCCCGAG 682
Db 568 GCCAGTACACCGCTAAGCCATGGAGCAGATGGCAGGTCGATGAGCAGCGCAGAG 627

QY 683 GCCATGGAGGTGGCCAGCCAGCCAGGAGGAGATGTTGCGAGGCCATGAGGACCATCGGCACC 742
Db 628 GCCATGGAGGTGCTAGTAAAGCTAGGAGGAGATGTTGAGGCAATGAGAACCATTTGGGACC 687

QY 743 CACCCACGACGAGCGCGGCTGAGAACCGACCTGCTGGAGAACCTGCGAGGCTTACCAG 802
Db 688 CACCCTAGCTCCAGTGGCGGTTTGAAGAGATGATCTCTTTGAAATTTTTCAGGCGCTACCAG 747

QY 803 AAGCGCATGGCGGTGCAGATCAGCGCTTCAAGTGAAC 840
Db 748 AAA CGGATGGGAGTGCAAATGCAGCGATTCAGGTGATC 785

RESULT 14
US-10-371-525-13
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/ Sequence 13, Application US/10371525
/ Publication No. US20030203869A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John D.
/ APPLICANT: Hermanson, Gary G.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Ishioka, Glenn Y.
/ APPLICANT: Livingston, Brian
/ APPLICANT: Cheenut, Robert W.
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Expression Vectors for Stimulating an
/ TITLE OF INVENTION: Immune Response and Methods of Using the Same
/ FILE REFERENCE: 39963-20022.01
/ CURRENT APPLICATION NUMBER: US/10/371,525
/ PRIOR FILING DATE: 2003-02-21
/ PRIOR APPLICATION NUMBER: US 09/311,784
/ PRIOR FILING DATE: 1999-05-13
/ PRIOR APPLICATION NUMBER: US 60/085,751
/ PRIOR FILING DATE: 1998-05-15
/ NUMBER OF SEQ ID NOS: 463
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 13
/ LENGTH: 816
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
/ OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
/ OTHER INFORMATION: Influenza matrix protein gene
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (16)...(816)
/ OTHER INFORMATION: PADRE-Influenza matrix
US-10-371-525-13
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Query Match      56.6%; Score 477.4; DB 6; Length 816;
Best Local Similarity 75.6%; Pred. No. 3.1e-103;
Matches 592; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

QY 56 GCCTGTCCTGACCCAGACCTGGGCTAGCTGCTGACCGAGGTGGAGACCTAGCTGCTG 115
Db 34 GCCTGGAACCTGGAAGGCTGCGCTATGAGTCTTCTAAACCGAGGTGCGAAACGTACGTTCTC 93

QY 116 AGCATATATCCCGAGCGGCCCTTGAAGCGAGATCCGCCAGAGGCTGGAGAGCGTGTTC 175
Db 94 TCTATCATCCATCAGCGGCCCTTCAAAGCGAGATCCGCGAGACTTTGAGATGTTTTT 153

QY 176 GCGCGCAAGAACCCGACCTGGAGGTGCTGATGAGTGGCTGGAAGACAGGCCCATCTGT 235
Db 154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTTAAAGACAAGACCAATCCTG 213

QY 236 AGCCCCCTGACCAAGGCGATCCTGGGCTTCTGTTTCACTGACCTGACCGTCCCAGCGAGGC 295
Db 214 TCACCTCTGACTAAGGGAATTTTGGGTTTGTGTTCACTGCTCACCGTCCCGAGTGGAGCGA 273

QY 296 GGCCTGAGCGCGCGCTTCTGTCGAAACCGCTTGAACCGCAACGCGACGCGCCCAACAC 355
Db 274 GGACTGAGCGGTAGACATTTGTCGAATATGCCCCCTTAATGGGAATGGAGACCCCAACAC 333

QY 356 ATGACAAAGCCCGTGAAGCTGTACAGGAAGCTGAAGAGGAGATCACTTTCCAGCGGCC 415
Db 334 ATGACAGGCGCGTAACTATATCAAGAACTGAAGAGGGAATGACATTCATCGGAGCA 393

QY 416 AAGGAGATCAGCTGAGCTACAGCGCGCGCCCTGCGCAGCTGATGGGCTGATCTAC 475
Db 394 AAGGAAGTTGCACTCAGTTTACTCAACTGTTGCGCTTGCCTGCGATGGGTCTCATATAC 453

QY 476 AACAGGATGGCGCGCTGACCGACCGAGGTGCGCTTTCGCGCTGGTGTGCGCACCTGCGAG 535
Db 454 AACCGGATGGGAACAGTGACACAGAAAGTGGCTTTCGCTTGTATGTGCCACTTGTGAG 513

QY 536 CAGATCGCCGACAGCCAGCAGCCGAGCTACAGGAGATGGTGAACCAACCAACCCCTGT 595
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Db 514 CAGATTGCTGATGCCCAACATCGGTCCCAAGGCGATGGGGACTACCAACCAACCCACTA 573  
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Db 634 GCTGGATCAAGTGAAGCAGGCGCAGAGGCCATGGAAGTTCGCAAGTCAAGGCTAGACAAATG 693  
Qy 716 GTGCAGGCCATGAGGACCATCGGCACACCCAGCAGCAGCGCCGCTGAAGAACGAC 775  
Db 694 GTGCAGGCAATGAGGACAAATTGGGACTCACCTAGCTCCAGTGCAGGTCTAAAGATGAT 753  
Qy 776 CTGCTGGAGAACCTGCAGGCCCTACCAAGAGCGCATGGGCGGTGCAGATGCAGCGCTTCAAG 835  
Db 754 CTATTGAAATTTGCGAGGCTTACCAAGAACGGATGGGGTGCAGATGCAGCGATTCAAG 813  
Qy 836 TGA 838  
Db 814 TGA 816

## RESULT 15

US-10-371-069-13  
; Sequence 13, Application US/10371069  
; Publication No. US20030216342A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMUNE Inc.  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Cheesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; FILE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.10  
; CURRENT APPLICATION NUMBER: US/10/371,069  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR FILING DATE: US 09/078,904  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 816  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion  
; OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of  
; OTHER INFORMATION: Influenza matrix protein gene  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (16)...(816)  
; OTHER INFORMATION: PADRE-Influenza matrix  
; US-10-371-069-13

Query Match 56.6%; Score 477.4; DB 6; Length 816;  
Best Local Similarity 75.6%; Pred. No. 3.1e-103;  
Matches 592; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

Qy 56 GCCCTGGCCCTGACCCAGACCTGGGCTAGCTGTGACCGAGGTGGAGACCTAGCTGCTG 115  
Db 34 GCCTGGACCCCTGAAGGCTGCCGCTATGAGTCTTTAACCCGAGGTGGAACGTCAGTCTTC 93  
Qy 116 AGCATCATCCCGAGCGCCCTCTGAAGGCCGAGATCGCCAGAGCGTGGAGGACGTGTC 175  
Db 94 TCTATCATCCCATCAGGCGCCCTCTAAGCCCGAGATCGCGCAGAGACTTGAGGATGTTTTT 153

Qy 176 GCCGGCAAGAACACCCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACCGAGCCCACTCCTG 235  
Db 154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCTCCTG 213  
Qy 236 AGCCCTCTGACCAAGGGCATCTTGGGCTTCGTGTTTCACTGACCGTGGCCAGCGAGCGC 295  
Db 214 TCACCTCTGACTAAGGGAAATTTAGGGTTTGTGTTTCACTGACCGTTCACCGTGGCCAGTGGCGA 273  
Qy 296 GGCCTCAGCGCCCGCCGCTTCGTGCAAGACGCCCTGAAACGGCAACGGCGGACCCCAACAC 355  
Db 274 GGACTCGAGCGTAGACGATTTGTCCAAATGCCCATAATGGGAATGGAGACCCCAACAC 333  
Qy 356 ATGGAACAAGCCCTGAGCTGTACAGAGAGCTCAAGAGGGAGATCACTTCCACGGCGCC 415  
Db 334 ATGGAAGAGGCGATTTAAACTATTAAGAAGCTGAAGAGGGAAATGACATTTCCATGGAGCA 393  
Qy 416 AAGGAGATCAGCTGAGCTACAGCGCGCGCCCTGGCCAGCTGCATGGGCTGATCTAC 475  
Db 394 AAGGAAGTTGCACTCAGTTACTCAACTGGTGGCTTGCAGTTGCGTCTCATATAC 453  
Qy 476 AACAGATGGGCGCCGCTGACCAACGAGGTGGCTTCGGGCTGTGTGGCGCACTGCGAG 535  
Db 454 AACCGGATGGGAACAGTGACCAAGTGGCTCTTGGGCTAGTATGTGCACTTGTGAG 513  
Qy 536 CAGATGCCGACAGCCAGCAGCCGACGAGGATGGTGGCCAGCACCAACCGCCATGGAGCAGATG 595  
Db 514 CAGATTGCTGATGCCCAACATCGGTCCACAGCAGATGGCGACTACCAACCAACCCACTA 573  
Qy 596 ATCAGGCACGAGAACAGGATGGTGTGGCCAGCACCAACCGCCAGGCCATGGAGCAGATG 655  
Db 574 ATCAGGCATGAGAACAGATGGTACTAGCCAGCACTACGGCTAAGGCCATGGAGCAATG 633  
Qy 656 GCCGGCAGCAGCAGCAGCGCCCGCGGCGCATGGAGGTGGCCAGCCAGGCCAGCGAGATG 715  
Db 634 GCTGGATCAAGTGAAGTGGCGAGCGGCGCATGGAAGTTCGAAAGTCAGGCTAGACAAATG 693  
Qy 716 GTGCAGGCCATGAGGACCATCGGCACCCAGCAGCAGCGCCGCTGGAAGAACGAC 775  
Db 694 GTGCAGGCAATGAGGACAAATTTGGGACTCACCTAGCTTCCAGTGCAGGTCTTAAAGATGAT 753  
Qy 776 CTGCTGGAGAACCTGCAAGGCCCTACCAAGAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 835  
Db 754 CTATTGAAATTTGCAAGGCTTACCAAGAACGGATGGGGTGCAGATGCAGCGATTCAAG 813  
Qy 836 TGA 838  
Db 814 TGA 816

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Job time : 830.608 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:50:55 ; Search time 383.576 Seconds  
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Perfect score: 844  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues  
Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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12: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB\_seq4.\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB\_seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
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| 1          | 730.6 | 86.6        | 756    | 12    | US-11-131-479-27   |
| 2          | 686.8 | 81.4        | 759    | 12    | US-11-131-479-69   |
| 3          | 686.8 | 81.4        | 1050   | 12    | US-11-131-479-59   |
| 4          | 665.2 | 78.8        | 982    | 12    | US-11-131-479-61   |
| 5          | 664.8 | 78.8        | 759    | 12    | US-11-131-479-79   |
| 6          | 594.6 | 70.5        | 756    | 12    | US-11-131-479-28   |
| 7          | 488   | 57.8        | 756    | 12    | US-11-131-479-26   |
| 8          | 476.4 | 56.4        | 1027   | 12    | US-11-131-479-3    |
| 9          | 473   | 56.0        | 1305   | 12    | US-11-131-479-45   |
| 10         | 460.4 | 54.5        | 987    | 12    | US-11-155-478A-131 |
| 11         | 454   | 53.8        | 982    | 12    | US-11-131-479-60   |
| 12         | 454   | 53.8        | 4822   | 12    | US-11-131-479-95   |
| 13         | 454   | 53.8        | 5161   | 12    | US-11-131-479-101  |
| 14         | 454   | 53.8        | 5398   | 12    | US-11-131-479-91   |
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| 17         | 454   | 53.8        | 7798   | 12    | US-11-131-479-99   |
| 18         | 454   | 53.8        | 7798   | 12    | US-11-131-479-100  |
| 19         | 454   | 53.8        | 8442   | 12    | US-11-131-479-106  |
| 20         | 454   | 53.8        | 8442   | 12    | US-11-131-479-107  |

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| 21 | 454   | 53.8 | 8450 | 12 | US-11-131-479-104    | Sequence 104, App |
| 22 | 454   | 53.8 | 8450 | 12 | US-11-131-479-105    | Sequence 105, App |
| 23 | 447.6 | 53.0 | 1027 | 12 | US-11-155-478A-130   | Sequence 130, App |
| 24 | 401.8 | 47.6 | 629  | 9  | US-11-137-807-18     | Sequence 18, Appl |
| 25 | 72.8  | 8.6  | 2430 | 7  | US-10-649-457-3      | Sequence 3, Appl  |
| 26 | 71    | 8.4  | 2295 | 7  | US-10-649-457-1      | Sequence 1, Appl  |
| 27 | 70.8  | 8.4  | 1521 | 12 | US-11-129-442-22     | Sequence 22, Appl |
| 28 | 70.4  | 8.3  | 1683 | 12 | US-11-131-479-37     | Sequence 37, Appl |
| 29 | 68.4  | 8.1  | 1566 | 12 | US-11-131-479-33     | Sequence 33, Appl |
| 30 | 68.4  | 8.1  | 1566 | 12 | US-11-131-479-35     | Sequence 35, Appl |
| 31 | 67.4  | 8.0  | 5278 | 12 | US-11-124-602-2      | Sequence 2, Appl  |
| 32 | 67.4  | 8.0  | 5304 | 12 | US-11-124-602-1      | Sequence 1, Appl  |
| 33 | 66.4  | 7.9  | 3624 | 7  | US-10-755-092-6      | Sequence 6, Appl  |
| 34 | 65.2  | 7.7  | 1494 | 8  | US-10-763-712A-173   | Sequence 173, App |
| 35 | 64.8  | 7.7  | 1092 | 12 | US-11-014-842A-40    | Sequence 40, Appl |
| 36 | 63.4  | 7.5  | 1497 | 12 | US-11-131-479-24     | Sequence 24, Appl |
| 37 | 62.8  | 7.4  | 1218 | 9  | US-11-096-568A-12913 | Sequence 12913, A |
| 38 | 62    | 7.3  | 1913 | 9  | US-11-096-568A-23950 | Sequence 23950, A |
| 39 | 61.6  | 7.3  | 1815 | 9  | US-11-096-568A-22463 | Sequence 22463, A |
| 40 | 61    | 7.2  | 1909 | 9  | US-11-096-568A-24544 | Sequence 24544, A |
| 41 | 61    | 7.2  | 3468 | 7  | US-10-755-092-2      | Sequence 2, Appl  |
| 42 | 61    | 7.2  | 3468 | 7  | US-10-755-092-4      | Sequence 4, Appl  |
| 43 | 60.6  | 7.2  | 678  | 9  | US-11-187-622-11     | Sequence 11, Appl |
| 44 | 60.2  | 7.1  | 2250 | 12 | US-11-052-554A-532   | Sequence 532, App |
| 45 | 59.8  | 7.1  | 1325 | 9  | US-11-096-568A-1077  | Sequence 1077, Ap |

ALIGNMENTS

RESULT 1  
US-11-131-479-27  
; Sequence 27, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jmenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 27  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein  
US-11-131-479-27

|                       |       |   |          |            |    |        |     |
|-----------------------|-------|---|----------|------------|----|--------|-----|
| Query Match           | 86.6% | Score   | 730.6    | DB         | 12 | Length | 756 |
| Best Local Similarity | 98.1% | Pred. No.   | 6.1e-146 |            |    |        |     |
| Matches               | 739   | Conservative  | 0        | Mismatches | 14 | Indels | 0   |
| Qy                    | 83    | AGCTGTGTCACCGAGGTGGAGACCTAGCTGCTGAGCATCATCCCGCGGCCCTCGAAG | 142      |            |    |        |     |
| Db                    | 4     | AGCTGTGTCACCGAGGTGGAGACCTAGCTGCTGAGCATCATCCCGCGGCCCTCGAAG | 63       |            |    |        |     |
| Qy                    | 143   | GCCGAGATGCCCGAGGTGGAGACCTGTTCCCGGCAAGAACACCGACCTGGAGTG    | 202      |            |    |        |     |
| Db                    | 64    | GCCGAGATGCCCGAGGTGGAGACCTGTTCCCGGCAAGAACACCGACCTGGAGTG    | 123      |            |    |        |     |
| Qy                    | 203   | CTGATGAGTGGCTGAAGACCGGCCCATCTGAGCCCCCTGACCAAGGGCATCTGGGC  | 262      |            |    |        |     |
| Db                    | 124   | CTGATGAGTGGCTGAAGACCGGCCCATCTGAGCCCCCTGACCAAGGGCATCTGGGC  | 183      |            |    |        |     |



```
Qy 263 TTCTGTTTACCTTGAACGCTGCCAGGAGCGCGGCTGCGAGCGCCGCGCTTCTGTGAG 322
Db 184 TTCTGTTTACCTTGAACGCTGCCAGGAGCGCGGCTTCTGTGAG 243
Qy 323 AACGCCCTGACGCGCAACGCGGCGCCCAACAACTGACAGGCGCGTGAAGCTGTACAGG 382
Db 244 AACGCCCTGACGCGCAACGCGGCGCCCAACAACTGACAGGCGCGTGAAGCTGTACAGG 303
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGGAGATCACGCTGAGCTACAGCGCC 442
Db 304 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGGAGATCACGCTGAGCTACAGCGCC 363
Qy 443 GGGCCCTTGGCCAGCTGATGGGCTGATCTTCAACAGGATGGGCGCGGTGACCAACCGAG 502
Db 364 GGGCCCTTGGCCAGCTGATGGGCTGATCTTCAACAGGATGGGCGCGGTGACCAACCGAG 423
Qy 503 GTGGCCCTTGGCCAGCTGATGGGCTGATCTTCAACAGGATGGGCGCGGTGACCAACCGAG 562
Db 424 GTGGCCCTTGGCCAGCTGATGGGCTGATCTTCAACAGGATGGGCGCGGTGACCAACCGAG 483
Qy 563 CACAGGAGATGGTGAACCAACCAACCCCTGATCAGGCAACGAGAACAGGATGGTGTG 622
Db 484 CACAGGAGATGGTGAACCAACCAACCCCTGATCAGGCAACGAGAACAGGATGGTGTG 543
Qy 623 GCCAGCAACCCGCAAGGCGCATGGAGCAGATGGCGCGGAGCAGCAGGCGCGCCGAG 682
Db 544 GCCAGCAACCCGCAAGGCGCATGGAGCAGATGGCGCGGAGCAGCAGGCGCGCCGAG 603
Qy 683 GCCATGAGGTGGCAGCGCCAGCGCAGGATGGTGCAGGCGCATGGAGCAGGCGCGCCAG 742
Db 604 GCCATGAGGTGGCAGCGCCAGCGCAGGATGGTGCAGGCGCATGGAGCAGGCGCGCCAG 663
Qy 743 CACCCAGCAGCAGCGCGGCTGAAGAACACCTGCTGAGAGAACCTGCGAGGCGCTACAG 802
Db 664 CACCCAGCAGCAGCGCGGCTGAAGAACACCTGCTGAGAGAACCTGCGAGGCGCTACAG 723
Qy 803 AAGCGCATGGCGTGCAGATGCAGCGTTCAAG 835
Db 724 AAGAGGATGGCGTGCAGATGCAGAGGTTCAAG 756
```

## RESULT 2

```
US-11-131-479-69
; Sequence 69, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; PRIOR FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for M1 Gene from VR4760
US-11-131-479-69
```

```
Query Match 81.4%; Score 686.8; DB 12; Length 759;
Best Local Similarity 94.4%; Pred. No. 1.1e-136;
Matches 712; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Qy 85 CCTGCTGACCGAGGTGGAGACCTAGCTGCTGAGCATCATCCCGAGCGGCCCTTGAGGCG 144
```

```
Db 6 CCTGCTGACAGAGTGGAAACATACGTGCTGAGATCGTCCCGAGCGGCCCTTGAGAGGC 65
Qy 145 CGAGATCGCCCGAGGCTGGAGGACGTGTTTCGCGCGCAAGAACACCGACCTGGAGGTGCT 204
Db 66 CGAGATCGCCCGAGGCTGGAGGACGTGTTTCGCGCGCAAGAACACCGACCTGGAGGCGCT 125
Qy 205 GATGGAGTGGCTGAAGACCAAGGCGCCATCTCTGAGCGCCCTTGAACAAAGGCAATCTTGGGCTT 264
Db 126 GATGGAGTGGCTGAAGACCAAGGCGCCATCTCTGAGCGCCCTTGAACAAAGGCAATCTTGGGCTT 185
Qy 265 CGTGTTCACCTTACCGTGCAGCGCGGCTGCGAGCGCGCGCTTCTGTGACAGAA 324
Db 186 CGTGTTCACCTTACCGTGCAGCGCGGCTGCGAGCGCGGCTGCGAGAGAGATTCGTGACAGAA 245
Qy 325 CGCCCTTGAACGGCAACCGCGGACCCCAACAACTGACAAAGCGCGCTGACAGAGAA 384
Db 246 CGCCCTTGAACGGCAACCGCGGACCCCAACAACTGACAAAGCGCGCTGACAGAGAA 305
Qy 385 GCTGAAGAGGAGATCACTTCCAGCGCGCAAGGAGATCAGCTGAGCTTACAGCGCGG 444
Db 306 GCTGAAGAGGAGATCACTTCCAGCGCGCAAGGAGATCAGCTTACAGCGCGG 365
Qy 445 CGCCCTTGGCAGCTGCATGGGCGCTGATCTTACAAAGATGGCGCGCTGACCAACCGAGGT 504
Db 366 CGCCCTTGGCAGCTGCATGGGCGCTGATCTTACAAAGATGGCGCGCTGACCAACCGAGGT 425
Qy 505 GGCCTTGGGCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCGCAGCAGCGCAGCCA 564
Db 426 GGCCTTGGGCTGGTGTGCGCCACCTGCGAGCAGATCGCCGACAGCGCAGCGCAGCCA 485
Qy 565 CAGGAGATGGTGAACCAACCAACCCCTGATCAGGACGAGAACAGGATGGTGTGCG 624
Db 486 CAGGAGATGGTGGCCACCAACCAACCCCTGATCAGACACGAGAACAGGATGGTGTGCG 545
Qy 625 CAGCACCACCGCAAGGCCATGGAGCAGATGGCGCGCAGCAGGAGCGCGCGCGAGGC 684
Db 546 CAGCACCACCGCAAGGCCATGGAGCAGATGGCGCGCAGCAGGAGCGCGCGCGAGGC 605
Qy 685 CATGGAGGTGGCCAGCGCAGGCGCAGGAGATGGTGCAGGCGCATGAGGACCATCGGACCCA 744
Db 606 CATGGAGATCGCCAGCCAGCGCAGCAGCAGATGGTGCAGGCGCATGAGGACCATCGGACCCA 665
Qy 745 CCCAGCAGCAGCGCGCGCTGAAGAACGACCTGCTGGAGAACCTGAGCGCTTACCGAGAA 804
Db 666 CCCAGCAGCAGCGCGCGCTGAAGAACGACCTGCTGGAGAACCTGAGCGCTTACCGAGAA 725
Qy 805 GCGCATGGCGCTGCAGATGCAGCGCTTCAAGTGA 838
Db 726 GAGATGGCGCTGCAGATGCAGAGATTCAGAGTGA 759
```

## RESULT 3

```
US-11-131-479-59
; Sequence 59, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; PRIOR FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
; LENGTH: 1050
```



```

; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for the M2M1 Fusion from VR4755
US-11-131-479-59

Query Match      81.4%; Score 686.8; DB 12; Length 1050;
Best Local Similarity 94.4%; Pred. No. 1.1e-136;
Matches 712; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 85 CCTGCTGACCGAGGTGGAGACCTAGCTGTGAGCATCATCCACAGCGGCCCTCTGAAGGC 144
Db 297 CTTGCTGACAGAGTGGAAACATACGTGTGAGCATCTGTGCCACAGCGGCCCTCTGAAGGC 356
Qy 145 CGAGATCCGCCAGAGGCTGGAGGAGCTGTTCGCCGGCAAGAACACCGACCTGGAGGTCCT 204
Db 357 CGAGATCCGCCAGAGCTGGAGGAGCTGTTCGCCGGCAAGAACACCGACCTGGAGGCCCT 416
Qy 205 GATGAGTGGCTGAAGACAGGCCCATCTGAGCCCCCTGACCAAGGGCATCTCTGGGCTT 264
Db 417 GATGAGTGGCTGAAGACAGGCCCATCTGAGCCCCCTGACCAAGGGCATCTCTGGGCTT 476
Qy 265 CTTGTTACCTGACCGTGGCCAGGAGCGGCGCTGAGCGCGCGCTGAGCGCGCGCTTCTGTCAGAA 324
Db 477 CTTGTTACCTGACCGTGGCCAGGAGGCGCTGAGCGCGCGCTGAGCGCGCGCTTCTGTCAGAA 536
Qy 325 CGCCCTGAACGGCAACGGCGACCCCAACAATGGACAAGCGCGTGAAGCTGTACAGAA 384
Db 537 CGCCCTGAACGGCAACGGCGACCCCAACAATGGACAAGCGCGCTGTACAGAA 596
Qy 385 GCTGAAGAGGAGATCACTTCCAGCGGCCAAGGAGATCAGCTTGAAGCTGACAGCGCGG 444
Db 597 GCTGAAGAGAGATCACTTCCAGCGGCCAAGGAGATCAGCTTGAAGCTGACAGCGCGG 656
Qy 445 CGCCCTGCGCAGCTGATGGGCTGATCTTAACAAGATGGGCGCGCTGACACAGAGGT 504
Db 657 CGCCCTGCGCAGCTGATGGGCTGATCTTAACAAGATGGGCGCGCTGACACAGAGGT 716
Qy 505 GGCCTTCGGCTGTGGTGGCCACCTGCGAGCAGATCGCCGACAGCCAGCCAGCCAGCCA 564
Db 717 GGCCTTCGGCTGTGGTGGCCACCTGCGAGCAGATCGCCGACAGCCAGCCAGCCAGCCA 776
Qy 565 CAGGAGATGTGTGACCAACCAACCCCTGATCAGGCAAGGAGCAAGGATGGTGTCTGGC 624
Db 777 CAGGAGATGTGTGACCAACCAACCCCTGATCAGGCAAGGAGCAAGGATGGTGTCTGGC 836
Qy 625 CAGCAACCGCCAAAGGCCATGGAGCAGATGGCGGCAAGCAGGAGCGCGCGCGAGGC 684
Db 837 CAGCAACCGCCAAAGGCCATGGAGCAGATGGCGGCAAGCAGGAGCGCGCGCGAGGC 896
Qy 685 CATGGAGGTGGCCAGCCAGGCGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCA 744
Db 897 CATGGAGATCGCCAGCCAGGCGCAGACAGATGGTGCAGGCCATGAGGACCATCGGCACCCA 956
Qy 745 CCCAGCAGCAGCGCGCGCTGAAGAACAGCCTGTGGAGAACCTTGACAGGCTTACCAAGAA 804
Db 957 CCCAGCAGCAGCGCGCGCTGAGGAGCAGCTTCTGTGAGAACCTTGACAGCCTTACCAGAA 1016
Qy 805 GCGCATGGCGGTGCAGATGCAAGCGCTTCAAGTGA 838
Db 1017 GAGAAATGGCGGTGCAGATGCAAGATTCAGATGA 1050
```

RESULT 4

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US-11-131-479-61
; Sequence 61, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
```

```

; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Codon Optimized Segment 7 from VR4763
US-11-131-479-61
```

```

Query Match      78.8%; Score 665.2; DB 12; Length 982;
Best Local Similarity 92.3%; Pred. No. 4.2e-132;
Matches 700; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 83 AGCCTGCTGACCGAGGTGGAGACCTAGCTGTGAGCATCATCCACAGCGGCCCTCTGAAG 142
Db 4 AGCCTGCTGACCGAGGTGGAACAGTATGTTCTCTATCGTGGCCAGCGGCCCTCTGAAG 63
Qy 143 GCCGAGATCGCCCAAGAGCTGGAGGAGCTGTTCGCCGGCAAGAACACCGACCTGGAGGTG 202
Db 64 GCCGAGATCGCCCAAGAGCTGGAGGAGCTGTTCGCCGGCAAGAACACCGACCTGGAGGCC 123
Qy 203 CTGATGAGTGGCTGAAGACAGGCCCATCTGTAGCCCCCTTGACCAAGGGCATCTCTGGGC 262
Db 124 CTGATGAGTGGCTGAAGACAGGCCCATCTGTAGCCCCCTTGACCAAGGGCATCTCTGGGC 183
Qy 263 TTCTGTTTCACTGACCGTGGCCAGCGAGCGCGCTGAGCGCGCGCTTCTGTGCAG 322
Db 184 TTCTGTTTCACTGACCGTGGCCAGCGAGAGGCGCTGACAGAAAGATTCGTGCAG 243
Qy 323 AACCCCTGAACGGCAACGGCGACCCCAACAATGACAGAGGCGCTGAGCTGTACAGG 382
Db 244 AACCCCTGAACGGCAACGGCGACCCCAACAATGACAGAGCGCTGAGCTGTACAGA 303
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGGCCAAGGAGATCAGCTTGAAGTACAGCGCC 442
Db 304 AAGCTGAAGAGAGATCACCTTCCAGCGGCCAAGGAGATCGCCCTGAGCTACAGCGCC 363
Qy 443 GGCGCCCTGCGCAGCTGCTGAGGCGCTGATCTACAGAGGATGGCGCGCGCTGACACCGAG 502
Db 364 GGCGCCCTGCGCAGCTGCTGAGGCGCTGATCTACAGAGATGGCGCGCGCTGACACCGAG 423
Qy 503 GTGSCCTTCGCGCTGTGGTGGCCACCTGCGAGCAGATCGCCGACAGCAGCAGCCGAGC 562
Db 424 GTGSCCTTCGCGCTGTGGTGGCCACCTGCGAGCAGATCGCCGACAGCAGCAGAGC 483
Qy 563 CACAGGAGATGTGTGACCAACCAACCCCTTGTATCAGGCAAGGAGATGATGATGATG 622
Db 484 CACAGAGATGTGTGGCCACCAACCCCTTGTATCAGACACAGAGAACAGATGATGATG 543
Qy 623 GCGAGCAACCGCCAAAGGCCATGGAGCAGATGGCGCGGAGCAGCAGGAGCGCGCGAG 682
Db 544 GCGAGCAACCGCCAAAGGCCATGGAGCAGATGGCGCGGAGCAGCAGGAGCGCGCGAG 603
Qy 683 GCCATGGAGTGGCCAGCGCCAGGCGCAGATGGTGCAGGCCATGAGGACCATCGGCAGCC 742
Db 604 GCCATGGAGTGGCCAGCGCCAGGCGCAGATGGTGCAGGCCATGAGGACCATCGGCAGCC 663
Qy 743 CACCCAGCAGCAGCGCGCGCTGAAGAACGACCTGTCTGGAGAACCTGCGAGGCGCTTACAG 802
Db 664 CACCCAGCAGCAGCGCGCGCTGAAGAGATGATCTTCTTGAAGATTTTGCAGACCTATCAG 723
Qy 803 AAGCGCATGGCGGTGCAGATGCAAGCGCTTCAAGTGAAC 840
Db 724 AACCGAATGGGGGTGCAGATGCAACGATGCAAGTGACC 761
```

```
RESULT 5
US-11-131-479-79
; Sequence 79, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Optimized M1 Coding Region
US-11-131-479-79

Query Match      78.8%; Score 664.8; DB 12; Length 759;
Best Local Similarity 92.5%; Pred. No. 5.2e-132;
Matches 699; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy      83 AGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATATCCCGAGCGGCCCTCTGAAG 142
Db      4 AGCTGCTGACCGAGGTGGAGACCTATGTTCTCTATCTGTCGCCAGCGGCCCTCTGAAG 63

Qy      143 GCCAGATCGCCAGAGCTGGAGACGTGTTCCGCGGCAAGACACCGACCTGGAGGTG 202
Db      64 GCCAGATCGCCAGAGCTGGAGACGTGTTCCGCGGCAAGACACCGACCTGGAGGTG 123

Qy      203 CTGATGAGTGGCTGAGACGACCTCTGAGCGCCCTTGACCAAGGGGATCTCTGGGC 262
Db      124 CTGATGAGTGGCTGAGACGACCTCTGAGCGCCCTTGACCAAGGGGATCTCTGGGC 183

Qy      263 TTGCTGTTTACCTTACCGTCCAGAGAGCGCGCTGACAGCGCGCGCTTCTGTGCAG 322
Db      184 TTGCTGTTTACCTTACCGTCCAGAGAGCGCGCTGACAGAGAAAGATTCTGTGCAG 243

Qy      323 AACGCCCTGAACGGGACGCGACCCCAACATGAGCAAGGCGCTGAGCTGTACAGG 382
Db      244 AACGCCCTGAACGGGACGCGACCCCAACATGAGCAAGGCGCTGAGCTGTACAGG 303

Qy      383 AAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGAGATCAGCTGAGCTACAGGCC 442
Db      304 AAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGAGATCAGCTGAGCTACAGGCC 363

Qy      443 GCGCCCTTGGCAGCTGATGAGATGAGCGCGCTGATCAACAGGATGGCGCGCTGACCAACCGAG 502
Db      364 GCGCCCTTGGCAGCTGATGAGATGAGCGCGCTGATCAACAGGATGGCGCGCTGACCAACCGAG 423

Qy      503 GTGGCTTGGCGCTGGTGGCGACCTCTGAGCGAGCATGCGCGGACAGCGACCGAGC 562
Db      424 GTGGCTTGGCGCTGGTGGCGACCTCTGAGCGAGCATGCGCGGACAGCGACCGAGC 483

Qy      563 CACAGGAGATGGTGACCAACCAACCCCTGTATCAGGACGAGAAAGGATGGTGTG 622
Db      484 CACAGAGATGGTGGCCCAACCAACCCCTGTATCAGAGACAGAAAGGATGGTGTG 543

Qy      623 GCCAGCACCAACCGCAAGGCTATGAGAGATGGCGCGCGAGCAGCGAGCGCGCGAG 682
Db      544 GCCAGCACCAACCGCAAGGCTATGAGAGATGGCGCGCGAGCAGCGAGCGCGCGAG 603

Qy      683 GCCATGGAGGTGGCCAGCGCCAGGCGAGATGGTGTGAGGCCATGAGGACCATCGGCACC 742
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Db      604 GCCATGGAGATCCCGAGCGCCAGACAGATGGTGTGAGGCCATGAGAGCCATCGGCACC 663
Qy      743 CACCCAGCAGCAGCGCGCCCTGTAAGAACGACCTCTGTGGAGAACCTGTGAGGCTTACCAG 802
Db      664 CACCCAGCAGCAGCGCGCCCTGTAAGATGATCTTCTTGAATAATTGACAGACCTATCAG 723

Qy      803 AACGGCATGGCGTGCAGATGACGCGCTTCAAGTGA 838
Db      724 AAACGAATGGGGTGCAGATGCAACGATTCAGTGA 759

RESULT 6
US-11-131-479-28
; Sequence 28, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-28

Query Match      70.5%; Score 594.6; DB 12; Length 756;
Best Local Similarity 86.9%; Pred. No. 3.8e-117;
Matches 654; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Qy      83 AGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATATCCCGAGCGGCCCTCTGAAG 142
Db      4 AGCTGCTGACGAGGTGGAGACGTACGTGCTGTCCATCATTCCTCAGGCCCTCTGAAG 63

Qy      143 GCCAGATCGCCAGAGGTGGAGACGTGTTCCGCGGCAAGACACCGACCTGGAGGTG 202
Db      64 GCCAGATTCGCCAGAGACTGGAGAGCTTTCGCGGCAAGAACACCGATCTGGAGGTG 123

Qy      203 CTGATGAGTGGCTGAGACGACCTCTGAGCGCCCTTGACCAAGGGGATCTCTGGGC 262
Db      124 CTGATGAGTGGCTGAGACCTCTGAGCGCCCTTGACCAAGGGGATCTCTGGGC 183

Qy      263 TTGCTGTTTACCTTACCGTCCAGAGCGCGCTGAGCGCGCGCTTCTGTGCAG 322
Db      184 TTGCTATTTACCTGACCGTCCCTCCGAGAGAGGCTGCGAGCGGAGGATTCTGTTTCAG 243

Qy      323 AACGCCCTGAACGGGACGCGACCCCAACATGAGCAAGGCGCTGAGCTGTACAGG 382
Db      244 AACGCCCTGAACGGGACGCGATCCCAACATGATGAGCGCTGAGCTGTATAGA 303

Qy      383 AAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGAGATCAGCTGAGCTACAGGCC 442
Db      304 AAGCTGAAGCGAGAGATCACATTTCATGGCGCCAAGAGATATCGCTGAGCTACAGTGC 363

Qy      443 GCGCCCTTGGCAGCTGATGAGATGAGCGCGCTGATCAACAGGATGGCGCGCTGACCAACCGAG 502
Db      364 GCGCCCTTGGCTTCTTGCATGGGCTGATATCAACAGAAATGGGCGCGCTTACTACAGAG 423

Qy      503 GTGGCTTGGCGCTGGTGTGCGACCTCTGAGCGAGCATGCGCGGACAGCGACCGAGC 562
```

|     |    |  |     |
|-----|----|--|-----|
| 424 | Db | GTAGCCTTTGGCCTGGTCTGCGCCACTTGGCGAGCAGATCGCCGACTCTCAGCAATAGATCT | 483 |
| 563 | Qy | CACAGCAGATGGTGACCAACCAACCCCTGATCAGGCAACGAGAAACAGATGGTGCTG      | 622 |
| 484 | Db | CACAGCAGATGGTGACCACTCAAAACCCCTGATCGGCAACGAGAAACAGATGGTGCTG     | 543 |
| 623 | Qy | GCCAGCACACCGCCAAAGCCATGAGCAGATGCCCGCAGCAGCAGAGCGCCGCCGAG       | 682 |
| 544 | Db | GCTCTTACTTACCGCCAAAGCCATGGAGCAGATGGCCCGCAGCATGAGCAGGCCGCCGAG   | 603 |
| 683 | Qy | GCCATGGAGGTGGCCAGCCAGGCGCAGATGGTGACGCCATGGAGACCATCGGCACC       | 742 |
| 604 | Db | GCCATGGAGGTAGCTTCAACAGSCCAGGCGAGATGGTGACGSCCATTCGAAACCATCGGCAC | 663 |
| 743 | Qy | CACCCACAGCAGAGCGCGGCTGAAGAACCACTGCTGGAGAACCTGAGGCGCTTACCAG     | 802 |
| 664 | Db | CACCCCTCAGCTCTTGCCGGGCTGAAGAACCACTGCTGGAGAACCTGCGAGGCGCTTACAG  | 723 |
| 803 | Qy | AAGCGCATGGCGTGCGAGATGACGCGCTTCAAG                              | 835 |
| 724 | Db | AAGAGAAATGGGGTTACAGATGACAGAGTTTCAAG                            | 756 |

```

RESULT 7
US-11-131-479-26
; Sequence 26, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EN/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-26

```

|  |     |  |     |
|--|-----|--|-----|
| Qy   | 383 | AAAGCTGAAGAGGAGATACCTTTCCACGGCGCCCAAGAGAGATCAGCCTGAGCTACAGGCC  | 442 |
|  |     |  |     |
| Db   | 304 | AAATTAAAGCGGAGATAACCTTCATGGAGCCAAAGAGATCTCCCTGTCTTACTCTGCA     | 363 |
|  |     |  |     |
| Qy   | 443 | GGCGCCTTCCAGCTGCATGGCGCTGATCTACAACAGGATGGCGCGCTGACCAACCCGAG    | 502 |
| Db   | 364 | GGTGCTCTCGCTCGTGTATGGGACTTATCTACAACCGAATGGCGCGCTCAACAACAA      | 423 |
|  |     |  |     |
| Qy   | 503 | GTGGCCTTCCGGCTGTGTGTCGCGCAACTCGGAGCAGATCGCCGACAGCCAGCACCGCAGC  | 562 |
| Db   | 424 | GTGGCTTTCGGGCTGTGTGTCGCGCAACTTGGCAACAGATTGCTGACAGTCAGCACCGGTCC | 483 |
|  |     |  |     |
| Qy   | 563 | CACAGGAGATGTGACCAACCAACCCCTGATCAGGCACGAGAACAGATGGTGTCTG        | 622 |
| Db   | 484 | CACCGTCMAATGGTCCACCACCAATCCGCTGATTAGACATGAAAAATCGCATGGTTCTA    | 543 |
|  |     |  |     |
| Qy   | 623 | GCCAGCACCAACCCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCAGCAGGCGCCCGCAG   | 682 |
| Db   | 544 | GCATCAACTACAGCCAAAGCAATGGAAACAATGGCCGGAAGCTCCGAGCAGGCTGCCGAG   | 603 |
|  |     |  |     |
| Qy   | 683 | GCCATGGAGTGGCCAGCCAGCCAGCGCAGATGGTGCAGGCCCATGAGGACCATCGGCACC   | 742 |
| Db   | 604 | GCAATGGAGTGGCGTCCAGGCCAGACAGATGGTACAGGCTATGAGAACTATCGGTACG     | 663 |
|  |     |  |     |
| Qy   | 743 | CACCCACGACGAGCGCCCGCTGAAAGACGACCTGCTGGAGAACCTGCGAGGCTACCGAG    | 802 |
| Db   | 664 | CACCCAAGTCTTTTCAGCTGGGCTGAAGNATGATCTTCTTGAGAACTCTGCAGGCTACCAA  | 723 |
|  |     |  |     |
| Qy   | 803 | AAGCGCATGGCGTGCAGATGCAGCGCTTCAA                                | 834 |
| Db   | 724 | AAGCGATGGCGTCCAGATGCAGAGATTAA                                  | 755 |
|  |     |  |     |
| RESULT 8   |     |  |     |
| US-11-131-479-3  |     |  |     |
| ; Sequence 3, Application US/11131479  |     |  |     |
| ; Publication No. US20060024670A1  |     |  |     |
| ; GENERAL INFORMATION:   |     |  |     |
| ; APPLICANT: Luke, Catherine J.  |     |  |     |
| ; APPLICANT: Vilalta, Adrian   |     |  |     |
| ; APPLICANT: Wloch, Mary K.  |     |  |     |
| ; APPLICANT: Evans, Thomas G.  |     |  |     |
| ; APPLICANT: Geall, Andrew J.  |     |  |     |
| ; APPLICANT: Jimenez, Gretchen   |     |  |     |
| ; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use |     |  |     |
| ; FILE REFERENCE: 1530.0640002/EJH/J-H                                       |     |  |     |
| ; CURRENT APPLICATION NUMBER: US/11/131,479                                  |     |  |     |
| ; CURRENT FILING DATE: 2005-05-18  |     |  |     |
| ; PRIOR APPLICATION NUMBER: US 60/571,854                                    |     |  |     |
| ; PRIOR FILING DATE: 2004-05-18  |     |  |     |
| ; NUMBER OF SEQ ID NOS: 112  |     |  |     |
| ; SOFTWARE: PatentIn version 3.3   |     |  |     |
| ; SEQ ID NO 3  |     |  |     |
| ; LENGTH: 1027   |     |  |     |
| ; TYPE: DNA  |     |  |     |
| ; ORGANISM: Influenza A virus  |     |  |     |
| US-11-131-479-3  |     |  |     |

Db 149 CTCATGAATGGCTAAAGACAGACCACATCTCTGCACCTCTGACCTAAGGGATTTTAGGA 208  
Qy 263 TTGCTGTTTACCCCTGACCGTSCCAGCAGCGCGCCCTGACGCGCCCGCTTCGTGCAG 322  
Db 209 TTTGTGTTTACCGCTCAACCGTGCCAGTGAGCGAGGACTGCGAGCGTGTGTCGAA 268  
Qy 323 AACGCCCTGAACGCCAAGCGGAGCCCAACACATGACACAGGCGGTGAAGCTGTACAGG 382  
Db 269 AATGCCCTTAATGGGAAACGGGGATCCAAATAACTGGAACAGCAGTTAACTGTATAGG 328  
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGGCCAAGAGATCAACCTGAGCTACAGCGCC 442  
Db 329 AAGCTCAAGAGGAGATAACATTCATGGGGCCAAAGAAATCTCACTCAGTTATCTGCT 388  
Qy 443 GCGCCCTTGGCAGCTGTCATGGGCTGATCTTACACAGAGATGGCGCGCTGACCAACCGAG 502  
Db 389 GGTGCACTTGCCAGTTGTATGGGCTCATATACAAAGGATGGGGCTGTGACCACTGAA 448  
Qy 503 GTGGCCTTGGCCTGTGTGGCCACCTGCGAGCAGATCGCCGACAGCAGCAGCAGCGAGC 562  
Db 449 GTGGCAATTTGGCCTGGTATGTGCAACCTGTGAACAGATTTGCTGACTCCCAAGCATCGTCT 508  
Qy 563 CACAGGAGATGGTGACCAACCAACCCCTGATCAGGCACGAGAACAGGATGGTCTG 622  
Db 509 CATAGGCAATTTGGTGACAAACCAATCCACTAATCAGACATGAGAACAGAAATGGTTTA 568  
Qy 623 GCCAGCACCAACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCCCGAG 682  
Db 569 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCGAGTGAAGCAGCAGAG 628  
Qy 683 GCCATGAGGTGGCCAGCCAGCCAGCAGCAGATGGTGAGGCCATGAGGACCATCGGCACC 742  
Db 629 GCCATGAGGTGTGCTAGTCAAGCTAGACAAATGGTGCAAGCGATGAGAACCATTTGGGACT 688  
Qy 743 CACCCAGCAGCAGCGCGGCTGAAGAACCACTGCTGGAGAACCTGCGAGCGCTACAG 802  
Db 689 CATCTAGCTCCAGTGTGCTGTGAAATATGATCTTTGAAATTTGCAGGCCCTATCAG 748  
Qy 803 AAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840  
Db 749 AACGAAATGGGGTGCAGATGCACAGGTTCAAGTGATC 786

## RESULT 9

US-11-131-479-45  
; Sequence 45, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 45  
; LENGTH: 1305  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Influenza A Virus M1 Fused to Synthetic HBcAg  
US-11-131-479-45

Query Match 56.0%; Score 473; DB 12; Length 1305;  
Best Local Similarity 76.8%; Pred No. 2,1e-91;  
Matches 578; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

Qy 83 AGCCTGCTGACCGAGGTGGAGACCTAGTGTCTGAGCATCATCCCGCGGCCCTTGAAG 142  
Db 4 AGTCTTTCTAACCGAGGTGCGAAACGTACGTACTCTCTATCATCTCCGTGAGCGCCCTCAAA 63  
Qy 143 GCGAGATGCCAGAGGCTGGAGGAGCTGTTCCGCGGCAAGAACACACCGACCTGGAGGTG 202  
Db 64 GCGAGATGCCAGAGACTTTGAAGATGTCTTTGCGAGGGAAGAACACTGATCTTGAGGTT 123  
Qy 203 CTGATGAGTGGTGAAGACCGGCCCATCTGAGCCCCCTGACCAAGGGGATCCTGGGC 262  
Db 124 CTCATGSAATGGCTAAAGACAAGACCAATCTGTCTGACCTCTGACTAAGGGGATTTAGGA 183  
Qy 263 TTGCTGTTTACCTGTACCGTGGCCAGGAGCGGGCTGACAGCGCCGCTTCGTGCAG 322  
Db 184 TTTGTGTTTACGCTACCGTGGCCAGTGAAGCGGAGCTGACGGGTAGACGCTTTGTCCAA 243  
Qy 323 AACGCCCTGAACGGCAACGGCGACCCCAACAAATGGACAAAGGCGGTGAAGCTGTACAGG 382  
Db 244 AATGCCCTTAATGGGAACGGGGATCCAAATAACTGGAACAAAGCAGTTAACTGTATAGG 303  
Qy 383 AAGCTGAAGAGGAGATCACCTTTCCAGCGGCCCAAGAGAGATCAGCCTGAGCTACAGGCC 442  
Db 304 AAGCTCAAGAGGAGATTAACATTTCCATGGGGCCAAAGAAATCTCACTCAGTTATCTGCT 363  
Qy 443 GCGCCCTGCGCAGCTGCTGCGCCTGATCTACAAAGGATGGCGCGCTGACCAACCGAG 502  
Db 364 GGTGCACTTCCAGTTGTATGGGCTCATATACAAAGGATGGGGCTGTGACCACTGAA 423  
Qy 503 GTGCGCTTCCGCTGTGTGCGCACCTGCGAGCAGATCGCCGACAGCCAGCAGCAGCGAGC 562  
Db 424 GTGCAATTTGGCTGTGTATGTGAACCTGTGAACAGATTTGCTGACTCCAGCATCGGTCT 483  
Qy 563 CACAGGAGATGGTGACCAACCAACCCCTGATCAGGCAACGAGAACGAGATGGTGTGCTG 622  
Db 484 CATAGGCAATTTGTGACAAACCAATCCACTAATCAGACATGAGAACAGATGGTTTAA 543  
Qy 623 GCGACACACCGCCAGGCGCATGAGCAGATGGCGGCGAGCAGCAGCGAGCGCGCGAG 682  
Db 544 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCGAGTGAAGCAGCAGAG 603  
Qy 683 GCCATGAGGTGGCGCAGCGCAGGCGAGCAGATGGTGAGGCCATGAGGACCATCGGCACC 742  
Db 604 GCCATGAGGTGTCTAGTCAAGCTAGACAAATGGTGACGGATGAGAACCATTTGGGACT 663  
Qy 743 CACCCAGCAGCAGCGCGCTGAAACACGACTGCTGGAGAACCTTGCAGGCGCTTACAG 802  
Db 664 CATCTAGTCCAGTGTGCTGCTGAAATATGATCTTCTGAAATTTTGCAGGCCCTATCAG 723  
Qy 803 AAGCGCATGGCGTGCAGATGCAGCGCTTCAAG 835  
Db 724 AACGAAATGGGGTGCAGATGCAACACGCTTCAAG 756

## RESULT 10

US-11-155-478A-131  
; Sequence 131, Application US/11155478A  
; Publication No. US20060014140A1  
; GENERAL INFORMATION:  
; APPLICANT: Boivin, Guy  
; APPLICANT: UNIVERSITE Laval  
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING  
; FILE REFERENCE: 6013-148US  
; CURRENT APPLICATION NUMBER: US/11/155,478A  
; CURRENT FILING DATE: 2005-06-20  
; PRIOR APPLICATION NUMBER: CA 2,411,264  
; PRIOR FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: CA 2,418,004  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994  
; PRIOR FILING DATE: 2003-12-19  
; NUMBER OF SEQ ID NOS: 174

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 987
; TYPE: DNA
; ORGANISM: human Influenza A virus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(987)
; OTHER INFORMATION: human Influenza A virus
; OTHER INFORMATION: strain A/Charlottesville/31/95 (H1N1)
; OTHER INFORMATION: accession number af398876
US-11-155-478A-131

```

| Query Match           | 54.5%          | Score 460.4   | DB 12    | Length 987 |
|-----------------------|----------------|---|----------|------------|
| Best Local Similarity | 75.5%          | Pred. No. 9.8e-89   |          |            |
| Matches 572           | Conservative 0 | Mismatches 186  | Indels 0 | Gaps 0     |
| Qy                    | 83             | AGCCTGCTGACCCGAGGTGGAGACCTAGTGTCTGAGCATCATCCCGAGCGGCCCTCTGAAG   | 142      |            |
| Db                    | 4              | AGTCTTCTAACCGAGGTGGAACGTAAGTCTCTCTATCGTCCGTGAGGCCCTCAA          | 63       |            |
| Qy                    | 143            | GCCGAGATCGCCAGAGGCTGGAGGACGTGTTCCGCGGCAAGAACACCGACTGTGAGGTG     | 202      |            |
| Db                    | 64             | GCCGAGATCGCACAGACTTTGAAGATGCTCTTTGCTGGAAGAAACACCGACTCTTGAGGCT   | 123      |            |
| Qy                    | 203            | CTGATGAGTGGCTGAAGACAGACGCCCATCTGTAGGCCCTCTGACCAAGGGCATCTGGGC    | 262      |            |
| Db                    | 124            | CTCATGAGTGGCTAAAGACAAGAACCGATCTCTGTACCTCTGACTAAGGGGATTTTAGGA    | 183      |            |
| Qy                    | 263            | TTCTGTGTTACCTTGACCTGCGGCCGAGCGCGCCCTGACGCGCGCGCTTGTGCGAG        | 322      |            |
| Db                    | 184            | TTTGTGTTACGCTCACGCTGCCAGTGAGCGAGGACTGCGAGCGTAGACGCTTGTGCCAA     | 243      |            |
| Qy                    | 323            | AACGCCCTGAACGGCAACGGGCAACCCAAACAATGGAACAAGGCGGTGAAGCTGTACAGG    | 382      |            |
| Db                    | 244            | AATGCCCTTAATGGGAATGGGGATCCAAATAACATGGAACAGACAGTTTAAACTGTATAGA   | 303      |            |
| Qy                    | 383            | AAGCTGAAGAGGGAGATCACCTTCCACGGGCCCAAGGAGATCAGCTGAGCTTACAGGCC     | 442      |            |
| Db                    | 304            | AAGCTTAAGAGGGAGATAAATTCATGCGGCCCAAGAAATAGCACTAGTTATCTGCT        | 363      |            |
| Qy                    | 443            | GGCGCCTTGGCCAGCTGCATGGGCGCTGATCTAACACAGGATGGGCGCGTGAACCAACGAG   | 502      |            |
| Db                    | 364            | GGTGCACTTGGCAGTTGTATGGGCGCTCATATACAAACAGATGGGGGCTGTGACCAACGAA   | 423      |            |
| Qy                    | 503            | GTGGCCTTGGCCTGGTGTGGCCACCTGCGAGCAGATCGCGGACAGCCAGCACCGCAGC      | 562      |            |
| Db                    | 424            | TCAGCAATTTGGCCTGATATGGCAACCTGTGAACAGATTGCTGACTCCAGCATTAAGTCT    | 483      |            |
| Qy                    | 563            | CACAGGCAGATGTGTACACCAACCAACCCCTGATCAGGCACGAGAACAGGATGGTGTG      | 622      |            |
| Db                    | 484            | CATAGGCNAATGGTAACAAACAACCAATCCATTAATAGACATGAGAACAGAAATGGTCTG    | 543      |            |
| Qy                    | 623            | GCCAGCAACCCGCAAGGCGCATGGAGCAGATGGCCGCGACAGACGAGCGCGCGCGAG       | 682      |            |
| Db                    | 544            | GCCAGCACTACAGCTAAAGCTATGGAGCAAAATGGCTGGATCGAGTGAACAAGACGACTGAG  | 603      |            |
| Qy                    | 683            | GCCATGAGGTGGCCAGCCAGCGCAGATGGTGCAGGCCCATGAGGACCATGGCACC         | 742      |            |
| Db                    | 604            | GCCATGAGGTGTGCTAGTCAGGCAGGCAAAATGGTGCAGGCAATGAGAGCCATTTGGGACT   | 663      |            |
| Qy                    | 743            | CACCCACAGCAGCGCGCGGCTTGAAGAAACGACCTGTGTGGAGAACCTTCAGGCGCTTACCAG | 802      |            |
| Db                    | 664            | CATCTAGCTCTAGCACTGGTCTGAAAAATGATCTTCTTGAAATTTGACGCGCTATACAG     | 723      |            |
| Qy                    | 803            | AAGGCATTGGCGTGCAGATGACGCGCTTCAAGTGAAC                           | 840      |            |
| Db                    | 724            | AAACGAATTGGGGTGCAGATGCAACGATTCAGGTGATC                          | 761      |            |

## RESULT 11

US-11-131-479-60

; Sequence 60, Application US/11131479

```

; Publication No. US20060024670A1
;
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H 479
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for Fragment 7 from VR4756
; US-11-131-479-60

```

| Query Match           | 53.8%          | Score 454   | DB 12    | Length 982 |
|-----------------------|----------------|---|----------|------------|
| Best Local Similarity | 74.9%          | Pred. No. 2.2e-87   |          |            |
| Matches 568           | Conservative 0 | Mismatches 190  | Indels 0 | Gaps 0     |
| Qy                    | 83             | AGCTGCTGACCGAGGTGGAGACTCAGTGTCTGAGCATCATCCCGAGCGGCCCTCTGAAG   | 142      |            |
| Db                    | 4              | AGCTTTCTAACCGAGGTGGAACGTATGTTCTCTATCGTTCCATCAGGCCCTCTCAA      | 63       |            |
| Qy                    | 143            | GCCGAGATCGCCACGAGGCTGGAGGACGTGTTTCGCCGCAAGAACACCGACTCTGGAGTG  | 202      |            |
| Db                    | 64             | GCCGAAATCGCGACGAGACTTGAAGATGCTTTTCTGGGAAAAACACAGATCTTGAGGCT   | 123      |            |
| Qy                    | 203            | CTGATGAGTGGCTGAAGACACAGGCCCATCTCTGAGCCCTCTGACCAAGGGCATCTGGGC  | 262      |            |
| Db                    | 124            | CTCATGNAATGGCTTAAAGACAAAGACCAATCTGTCACTCTGACTTAAGGGGATTTGGGG  | 183      |            |
| Qy                    | 263            | TTCGTGTTCACCTGACCGTGCCCGAGCGAGCGCGCTGACGCGCGCTTCGTGACAG       | 322      |            |
| Db                    | 184            | TTTGTGTTACGCTCAACCGTGCCAGTGAGCGAGACTGACGCTGTAAGACGCTTTGTCCAA  | 243      |            |
| Qy                    | 323            | AAGCCCTGAAACGGCAACGGCGACCCCAACAACTGGAACAAGGCCGTGAAGCTGTACAGG  | 382      |            |
| Db                    | 244            | AATGCCCTCAATGGGAATGGGATCCAAATPAACATGGACAGACAGTTAAACTATATAGA   | 303      |            |
| Qy                    | 383            | AAGCTGAAGAGGGAGATCACTTCCACGGCGCCAAAGGAGATCAGGCTGAGCTACAGCGCC  | 442      |            |
| Db                    | 304            | AAACTTAAGAGGGAGATTACATTCATGGGGCCAAAGAAATAGCACTCAGTTATTCTGTCT  | 363      |            |
| Qy                    | 443            | GGGCGCTTGCCAGCTGCATGGGCTGATCTACACAGGATGGGGCGCGTGACCAACCGAG    | 502      |            |
| Db                    | 364            | GGTGCACTTCGCAGTTGCATGGGCTCATATAACAACAGAAATGGGGGCTGTAAACCACTGA | 423      |            |
| Qy                    | 503            | GTGGCTTTGGGCTGTGTGGCCACCTCGACGACGATCGCGACAGCCAGCACCGCAGC      | 562      |            |
| Db                    | 424            | GTGGCTTTGGCTGTGTATGTGCAACATGTGAAACAGATTGTGACTCCAGCACAGGTCT    | 483      |            |
| Qy                    | 563            | CACAGGCAGATGTGTACCAACCAACCCCTGTATCAGGCACGAGAACAGGATGTGTCTG    | 622      |            |
| Db                    | 484            | CATAGGCAATGGTGGCAACCAACCAATCCATTAATTAAGGCATGAAACAGAAATGGTTTG  | 543      |            |
| Qy                    | 623            | GCACGACACACCGCAAGGCCATGGAGCAGATGGCGCGCAGCAGCGGACAGGCCCGCCAG   | 682      |            |
| Db                    | 544            | GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCAAGTGTAGCAGCAGCGGAG   | 603      |            |
| Qy                    | 683            | GCCATGAGTGGCCACCGAGCCAGCAGATGTGTGAGGCCATGTGAGGACCATCGCACCC    | 742      |            |
| Db                    | 604            | GCCATGAAATTTGCTAGTCAGCGCAGGCAATGGTGTGAGGCCAATGAGAGCCATTGGGACT | 663      |            |
| Qy                    | 743            | CACCCACGACGACGCGCGGCTTGAAGAAACGACCTGTCTGGAGAACCTCTGAGGCCTACCA | 802      |            |

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Db 664 CATCTAGCTCCAGTGTGGTCTAAAGATGATCTTCTTGAAATTTGCAGACCTATCAG 723
Qy 803 AAGCGCATGGCGTCGACAGATGCGCGCTTCAAGTGAAC 840
Db 724 AAACGAATGGGGTGCAGATGCAACGATTCAAGTGACC 761

RESULT 12
US-11-131-479-95
; Sequence 95, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4764, Ligation of VR4756 RV-Sali into VR10682 RV
US-11-131-479-95

Query Match 53.8%; Score 454; DB 12; Length 4822;
Best Local Similarity 74.9%; Pred. No. 2e-87;
Matches 568; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

Qy 83 AGCTGTCTGACCGAGGTGGAGACCTACGTGTGTAGACATCATCCCGCGGCCCTCGAAG 142
Db 817 AGCTTCTAACCGAGGTGGAACGTATGTTCTCTATCGTTCCATCAGGCCCTCAA 876

Qy 143 GCCAGATTCGCCAGAGCTGGAGAGCTGTTTCGCGGCAAGAAACACGACCTGGAGTG 202
Db 877 GCCGAAATCGCGCAGAGACTTGAAGATGCTTTCTGCGGAAAAACAGATCTTGAGGCT 936

Qy 203 CTGATGAGTGGCTGAAGACAGCGCCATCTGTAGCCCTTGACCAAGGCGATCTCGGC 262
Db 937 CTCATGGAATGGCTAAAGACAAGACCAATCTGTACCTCTGACTAAGGGGATTTTGGG 996

Qy 263 TTGCTGTTACCTCTGACCGTCCCGAGGAGCGCGCTTCGAGCGCCGCTTCGTGCAG 322
Db 997 TTTGTGTTACGCTCACTGCGTCCAGTGAGCGAGACTGTCAGCTAGACGCTTTGTCAA 1056

Qy 323 AACGCCCTGAACCGCAACCGCGACCCCAACAACTGACAGAGCGCTGTAAGCTGTACAG 382
Db 1057 AATGCCCTCAATGGGAATGGGGATCCAAATAACATGACAGAGCAGTTAAACTATAGA 1116

Qy 383 AAGCTGAAGGGAGATCACCTTCCAGCGCCCAAGAGATCAGCTTGAGCTACAGGCC 442
Db 1117 AAATTAAGAGGGAGATTAACATTCCATGGGGCCAAAGAAATAGCACTAGTTATCTGCT 1176

Qy 443 GCGCCCTTGGCGAGCTGATGGGCTGATCTACACAGAGATGGGCGCTGACCAACCGAG 502
Db 1177 GGTGCACTTGCAGTTGCATGGGCTCATATACAAAGAAATGGGGGCTGTAAACACTGAA 1236

Qy 503 GTGCGCTTGGCGCTTGGTGTGCGCACTCTGCGAGAGATTCGCGCAGCAGCGCAGC 562
Db 1237 GTGCGCTTGGCGCTTGGTGTGCAACATGTGAACAGATTTGACTCCACAGCAGGTCT 1296

Qy 563 CACAGGAGATGGTGAACACCAACCCCTGTATCGGACAGGACAGGATGGTGTG 622
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Db 1297 CATAGCAATGTGTGCAACCAACCAATCCATTAAAGGCATGAGAACAAGATGTTTG 1356
Qy 623 GCCAGACACCCCGCAAGGCCATGGAGCAGATGGCGCGAGAGCGAGCGAGCGCGCGAG 682
Db 1357 GCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGGATCAAGTGAGCAGCGAGCGAG 1416
Qy 683 GCCATGGAGTGGCCAGCGCAGCGCAGATGGTGCAGGCCATGAGGCCATTCGGCACC 742
Db 1417 GCCATGGAATTTGCTAGTCAGGCCAGGCAATGGTGCAGCAATGAGCCATTGGGACT 1476
Qy 743 CACCCAGCAGCAGCGCGCTGAAAGAACGACCTGCTGGAGAACCTGCGAGGCTTACAG 802
Db 1477 CATCTAGTCCAGTGTGCTTAAAGATGATCTTCTTGAAATTTGCAGACCTATCAG 1536
Qy 803 AAGCGCATGGCGTCGAGATGCGCGCTTCAAGTGAAC 840
Db 1537 AAACGAATGGGGTGCAGATGCAACGATTCAAGTGACC 1574

RESULT 13
US-11-131-479-101
; Sequence 101, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101
; LENGTH: 5161
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4770, M2 Insert Replacing WNV Insert in VR6430
US-11-131-479-101

Query Match 53.8%; Score 454; DB 12; Length 5161;
Best Local Similarity 74.9%; Pred. No. 2e-87;
Matches 568; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

Qy 83 AGCTGTGACCGAGGTGGAGACCTACGTGTGTAGACATCATCCCGAGCGGCCCTCGAAG 142
Db 1150 AGCTTCTTAACCGAGGTGGAACGTATGTTCTCTATCGTTCCATCAGGCCCTCAA 1209

Qy 143 GCCAGATTCGCCAGAGCTGGAGAGCTGTTTCGCGGCAAGAAACACGACCTGGAGTG 202
Db 1210 GCCGAAATCGCGCAGAGACTTGAAGATGCTTTGCTGGGAAAAACAGATCTTGAGCT 1269

Qy 203 CTGATGAGTGGCTGAAGACAGCGCCCATCTGTAGCGCCCTTGACCAAGGCGATCTCGGC 262
Db 1270 CTCATGGAATGGCTAAAGACAAGCAACATCTGTACCTCTGACTAAGGGGATTTTGGG 1329

Qy 263 TTGCTGTTACCTCTGACCGTGGCGAGCGCGCTGAGCGGCCCTGAGCGGCCCTTCGTGAG 322
Db 1330 TTTGTGTTACGCTCACTGCGTCCAGTGCAGGAGACTGCGCGGTAGCGGTAGACGCTTTGTCAA 1389

Qy 323 AAGCCCTGAACCGCAACCGCGACCCCAACAACTGACAGAGCGCTGGAAGCTGTACAGG 382
Db 1390 AATGCCCTCAATGGGAATGGGATCCAAATAACATGACAGAGCAATTAACATATAGA 1449

Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGAGATCAGCTTGAGCTACAGGCC 442
Db 1450 AAATTAAGAGGGAGATTAACATTCCATGGGGCCAAAGAAATAGCACTCAGTTATCTGCT 1509
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Qy 443 GCGCCCTGGCAGCTGCATGGGCTGATCTACAAAGATGGGCGCGTGCACACGAG 502  
Db |||||  
1510 GGTGACCTTGCAGTTGCATGGGCTCATATACAAAGATGGGCGCTGTAACCACTGAA 1569  
Qy 503 GTGGCTTGGCCTGGTGTGGCCACCTGCGAGCAGATGCGCGACAGCAGCAGCGAGC 562  
Db |||||  
1570 GTGGCTTGGCCTGGTGTGCAACATGTGAACAGATTTGCTGACTCCCGACACAGGTCT 1629  
Qy 563 CACAGGAGATGGTGACCAACACCAACCCCTGTATCAGGCACGAGAACAGGATGTCGTCG 622  
Db |||||  
1630 CATAGGCAATGGTGGCAACCAATCCATTAATAGGCATGAGAACAGATGGTTTG 1689  
Qy 623 GCCAGCACACCGCCCAAGCCATGGAGCAGATGGCGCGCAGCAGCAGCGCCGAG 682  
Db |||||  
1690 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCAAGTGAGCAGCGAG 1749  
Qy 683 GCCATGGAGTGGCCAGCCAGCCAGCAGGATGGTGCAGGCCATGAGGACCATCGGCAAC 742  
Db |||||  
1750 GCCATGGAAATTTGCTAGTCAGGCCAGGCAATGGTGCAGGCAATGAGAGCCATTTGGGACT 1809  
Qy 743 CACCCAGCAGCGCGCGCTGAAGAACGACCTGCTGGAGAACCTGCGAGACCTGCGAGCCATCCAG 802  
Db |||||  
1810 CATCTAGCTCCAGTGGCTTAAAGATGATCTTCTTGAATAATTTGCAGACCTATCAG 1869  
Qy 803 AAGCGCATGGCGTGCAGATCAGCGCTTCAAGTGAAC 840  
Db |||||  
1870 AAACGAATGGGGTGCAGATGCAGCATTCAGGTGACC 1907

## RESULT 14

US-11-131-479-91  
; Sequence 91, Application US/11131479  
; Publication No. US2006024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 91  
; LENGTH: 5398  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VR4756, Ligation of Segment7 into VR10551  
US-11-131-479-91

Query Match 53.8%; Score 454; DB 12; Length 5398;  
Best Local Similarity 74.9%; Pred. No. 2e-87;  
Matches 568; Conservative 0; Mismatches 190; Indels 0; Gaps 0;  
Qy 83 AGCCTGCTGACCGAGGTGGAGACCTACGTCGTGAGCATATCCCGCGGCCCTCGAAG 142  
Db |||||  
1655 AGCCTTCAACCGAGGTGGAACGATGTTCTCTATCGTTCAATGAGGCCCTCAA 1714  
Qy 143 GCCAGATCGCCAGAGCTGGAGACGTTGCGCGGCAAGAACACCGACCTGGAGGTG 202  
Db |||||  
1715 GCCGAATCGCGAGAGCTTGAAGATGTTCTGCTGGGAAACACAGATCTTGAGGCT 1774  
Qy 203 CTGATGGAGTGGTGAAGACGAGGCCCATCTCTGAGCCCTCGAACAGGAGCATCTGGGC 262  
Db |||||  
1775 CTCATGGAATGGCTAAAGACAGACCAATCTCTGTCACCTCTGACTAAGGGGATTTGGG 1834

Qy 263 TTGCTGTTCACTCCGTGACCGTCCCGAGCGAGCGCGGCTGCGAGGCCCGCTTCGTGAG 322  
Db |||||  
1835 TTTGTGTTCACTCCGTGACCGTCCCGAGTGCAGGAGTGCAGCGTAGACGCTTGTGCAA 1894  
Qy 323 AAGCCCTGAACGGCAAGCGGACCCCAACAAATGACAAAGCCGCTGAAGCTGTACAGG 382  
Db |||||  
1895 AATGCCCTCAATGGGAATGGGATGCCAAATAACATGACAGAGCAGTTAAACTATATAGA 1954  
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGAGATCAAGCTTGAGCTACAGGGCC 442  
Db |||||  
1955 AACTTAAGAGGAGATTAATTCATTCATGGGGCCAAAGAAATAGCACTCAGTTATCTGCT 2014  
Qy 443 GCGCCCTGCGCAGCTGCATGGGCTGATCTAACAAGATGGCGCGCTGACCAACCGAG 502  
Db |||||  
2015 GGTGCACTTGCCAGTTGCATGGGCTCATATACAAGAAATGGGGCTGTAACCACTGAA 2074  
Qy 503 GTGGCTTGGCCTGGTGTGGCCACCTGCGAGCAGATCCCGACAGCCAGCAGCCGAGC 562  
Db |||||  
2075 GTGGCTTGGCCTGGTGTGCAACATGTGAACAGATTTGCTGACTCCCAGCACAGGTCT 2134  
Qy 563 CACAGGAGATGGTGACCAACCAACCCCTGTATCAGGCAAGAGATGAGTGGTGTG 622  
Db |||||  
2135 CATAGGCAATGGTGGCAACCAATCCATTAATAGGCATGAGAACAGATGGTTTG 2194  
Qy 623 GCCAGCACCCCGCAGGCGCATGGAGCAGATGGCGCGCAGCAGCAGCGCCGAGC 682  
Db |||||  
2195 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCAAGTGAGCAGCGAG 2254  
Qy 683 GCATGAGTGGCCAGCCAGCGCAGCAGATGGTGCAGGCCATGAGGACCATCGGACCC 742  
Db |||||  
2255 GCCATGGAATTTGCTAGTCAGGCGCAGCAATGGTGCAGGCAATGAGAGCCATTTGGGACT 2314  
Qy 743 CACCCAGCAGCAGCGCGCTGAAGAACGACCTGCTGGAGAACCTGCGAGCCCTACCAG 802  
Db |||||  
2315 CATCTAGCTCCAGTGGTCTAAGATGATCTTCTTGAATAATTTGCAGACCTATCAG 2374  
Qy 803 AAGCGCATGGCGTGCAGATGCGCGCTTCAAGTGAAC 840  
Db |||||  
2375 AAACGAATGGGGTGCAGATGCAACGATTCAAGTGACC 2412

## RESULT 15

US-11-131-479-97  
; Sequence 97, Application US/11131479  
; Publication No. US2006024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 97  
; LENGTH: 7798  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VR4766, Ligation of Seg7 into VR4762  
US-11-131-479-97

Query Match 53.8%; Score 454; DB 12; Length 7798;  
Best Local Similarity 74.9%; Pred. No. 2e-87;  
Matches 568; Conservative 0; Mismatches 190; Indels 0; Gaps 0;  
Qy 83 AGCCTGCTGACCGAGGTGGAGACCTACGTCGTGAGCATCATCCCGAGCGGCCCTCGAAG 142





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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:02:13 ; Search time 190.994 Seconds  
(without alignments)  
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Perfect score: 942  
Sequence: 1 gcuuguuuuuugcagaag.....aaaaaaaaaaaaaaaaaaaaa 942

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 130357 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
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7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 764   | 81.1        | 4023   | 3     | US-08-809-513A-8   |
| 2          | 761.8 | 80.9        | 6802   | 3     | US-08-809-513A-6   |
| 3          | 695.8 | 73.9        | 1027   | 6     | PCT-US95-12357A-3  |
| 4          | 647.4 | 68.7        | 1023   | 3     | US-09-506-286B-1   |
| 5          | 647.4 | 68.7        | 1023   | 3     | US-09-762-861B-1   |
| 6          | 647.4 | 68.7        | 1023   | 3     | US-10-065-133A-1   |
| 7          | 647.4 | 68.7        | 1023   | 3     | US-10-434-811A-1   |
| 8          | 644.6 | 68.4        | 1023   | 3     | US-09-506-286B-4   |
| 9          | 644.6 | 68.4        | 1023   | 3     | US-09-762-861B-4   |
| 10         | 644.6 | 68.4        | 1023   | 3     | US-10-065-133A-4   |
| 11         | 644.6 | 68.4        | 1023   | 3     | US-10-434-811A-4   |
| 12         | 637.2 | 67.6        | 756    | 3     | US-09-506-286B-3   |
| 13         | 637.2 | 67.6        | 756    | 3     | US-09-762-861B-3   |
| 14         | 637.2 | 67.6        | 756    | 3     | US-10-065-133A-3   |
| 15         | 637.2 | 67.6        | 756    | 3     | US-10-434-811A-3   |
| 16         | 634.4 | 67.3        | 756    | 3     | US-09-506-286B-6   |
| 17         | 634.4 | 67.3        | 756    | 3     | US-09-762-861B-6   |
| 18         | 634.4 | 67.3        | 756    | 3     | US-10-065-133A-6   |
| 19         | 634.4 | 67.3        | 756    | 3     | US-10-434-811A-6   |
| 20         | 632.6 | 67.2        | 816    | 3     | US-09-311-784A-13  |
| 21         | 79    | 8.4         | 290    | 3     | US-10-131-827-8418 |
| 22         | 77.6  | 8.2         | 1097   | 3     | US-09-832-129-21   |
| 23         | 77.2  | 8.2         | 1069   | 3     | US-09-372-422A-7   |
| 24         | 76.8  | 8.2         | 569    | 3     | US-09-461-325-44   |

|    |      |     |      |   |                    |                   |
|----|------|-----|------|---|--------------------|-------------------|
| 25 | 76.8 | 8.2 | 569  | 3 | US-10-012-542-44   | Sequence 44, Appl |
| 26 | 76.8 | 8.2 | 569  | 3 | US-10-115-123-44   | Sequence 44, Appl |
| 27 | 76.8 | 8.2 | 3080 | 3 | US-09-099-041A-25  | Sequence 25, Appl |
| 28 | 76.8 | 8.2 | 3080 | 3 | US-09-245-281-25   | Sequence 25, Appl |
| 29 | 76.8 | 8.2 | 3080 | 3 | US-09-207-359B-25  | Sequence 25, Appl |
| 30 | 76.8 | 8.2 | 3080 | 3 | US-09-340-620A-25  | Sequence 25, Appl |
| 31 | 76.8 | 8.2 | 3080 | 3 | US-09-865-364-25   | Sequence 25, Appl |
| 32 | 76.8 | 8.2 | 3080 | 3 | US-09-728-721-25   | Sequence 25, Appl |
| 33 | 76   | 8.1 | 1733 | 3 | US-09-073-569-1    | Sequence 1, Appl  |
| 34 | 75.8 | 8.0 | 990  | 3 | US-09-800-729-79   | Sequence 79, Appl |
| 35 | 75.8 | 8.0 | 1934 | 3 | US-08-776-844-1    | Sequence 1, Appl  |
| 36 | 75.8 | 8.0 | 1934 | 3 | US-09-909-325-1    | Sequence 1, Appl  |
| 37 | 75.8 | 8.0 | 1934 | 3 | US-09-909-326-1    | Sequence 1, Appl  |
| 38 | 75.8 | 8.0 | 1985 | 3 | US-09-907-794A-212 | Sequence 212, App |
| 39 | 75.8 | 8.0 | 1985 | 3 | US-09-905-125A-212 | Sequence 212, App |
| 40 | 75.8 | 8.0 | 1985 | 3 | US-09-902-775A-212 | Sequence 212, App |
| 41 | 75.8 | 8.0 | 1985 | 3 | US-09-906-700-212  | Sequence 212, App |
| 42 | 75.8 | 8.0 | 1985 | 3 | US-09-903-603A-212 | Sequence 212, App |
| 43 | 75.8 | 8.0 | 1985 | 3 | US-09-904-920A-212 | Sequence 212, App |
| 44 | 75.8 | 8.0 | 1985 | 3 | US-09-909-064-212  | Sequence 212, App |
| 45 | 75.8 | 8.0 | 1985 | 3 | US-09-905-381A-212 | Sequence 212, App |

ALIGNMENTS

RESULT 1

US-08-809-513A-8  
; Sequence 8, Application US/08809513A  
; Patent No. 6524588  
; GENERAL INFORMATION:  
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette  
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a  
; TITLE OF INVENTION: Method  
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising  
; NUMBER OF SEQUENCE ADDRESSES: 9  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: NORRIS MCLAUGHLIN & MARCUS  
; STREET: 660 White Plains Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591-5144  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage  
; COMPUTER: Gateway Pentium II  
; OPERATING SYSTEM: Windows 98  
; SOFTWARE: Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,513A  
; FILING DATE: 24-MAR-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/03663  
; FILING DATE: 18-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94115505.3  
; FILING DATE: 30-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurt G. Briscoe  
; REGISTRATION NUMBER: 33,141  
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 332-1700  
; TELEFAX: (914) 332-1844  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4023 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO



|     |    |  |     |
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| 394 | Db | TTCTGCTGGTGACCTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGAC     | 453 |
| 472 | Qy | CACUGAAGUGGCACUUTUGGCCUGGUAUGUGCAACUGUGAACAGAUUGUCUGACUCCCGACGA  | 531 |
| 454 | Db | CACCTGAAGTGGCATTTGGCCTGGTATGTGTGCAACCTGTGAAACAGATTGCTGACTCCGACGA | 513 |
| 532 | Qy | UCGGUCUCUAGGGCAAAUUGUGUGACAAACCAACCCCAUAUACAGACAUGAGAAACAGAAU    | 591 |
| 514 | Db | TCGGTCTCATAGGCCAAATGGTGTGACCAACCAACCCCACTAATCAGACATGAGAACAGAAAT  | 573 |
| 592 | Qy | GGUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUGGCGUGGACUGAGUGAGCAAGC     | 651 |
| 574 | Db | GGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGGATCGGATCGAGCAAGC   | 633 |
| 652 | Qy | AGCAGAGGCCAUGGAGGUGUCUAGUCAGGCUAGGCAAAUGGUGCAAGCGGAUGAGAACCAU    | 711 |
| 634 | Db | AGCAGAGCCATGAGAGGTGCTAGTCAGGCTAGGCAAAATGGTGCAACGGATGAGAACCAT     | 693 |
| 712 | Qy | UGGGAUCUACUCCUAGCUCCAGUCUGUGUCUGAGAAAAUGAUUCUUCUGAAAAUUUGCAGGC   | 771 |
| 694 | Db | TGGGACTCATCTAGCTCCAGTCTGCTGTGTGAAAAATGCTCTTCTTGAAAAATTTGCAGGC    | 753 |
| 772 | Qy | CUAUCAGAAACGAAUGGGGUGCAGAUGCCAAACGCUUCAAUGUAAACUAGUACU           | 824 |
| 754 | Db | CTATCAAAACGAAATGGGGTGCAGATGCAACGGTTCAATGATCTCTCTCGCT             | 806 |

### RESULT 3

```

PCT-US95-12357A-3
; Sequence 3, Application PC/TUS9512357A
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: Nucleic Acid Encoding Mutant Matrix
; TITLE OF INVENTION: Proteins Useful for Attenuation or Enhancement of
; TITLE OF INVENTION: Influenza A Virus, Vaccines and Methods of making and
; TITLE OF INVENTION: Using Thereof
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12357A
; FILING DATE: 29-SEPT-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/316,419
; FILING DATE: 30-SEPT-1994
; CLASSIFICATION:
; APPLICATION NUMBER: 08/471,100
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.048PC01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION: At location 663, r = A or G; At amino
; -OTHER INFORMATION: location 213, xaa = Val
US-09-506-286B-1

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| Query Match           | 68.7%            | Score 647.4  | DB 3     | Length 1023 |
|-----------------------|------------------|--|----------|-------------|
| Best Local Similarity | 70.8%            | Pred. No. 8.1e-146   |          |             |
| Matches 546           | Conservative 148 | Mismatches 177   | Indels 0 | Gaps 0      |
| Qy                    | 46               | AGAUCAAAGAUGAGUCUUAUACCGAGGUGGAAACGUAAGUCUUAUACUACGCCGUC         | 105      |             |
| Db                    | 15               | ATATTTAAAGATGAGTCTTCTGA CCGAGGTGAAACGTACGTTCTCTCTATCTGTACCATC    | 74       |             |
| Qy                    | 106              | AGGCCCCUCUAAAGCGAGAUUCGCA CAGAGACUUAAGAUGUCUUAUAGGAGAAACAC       | 165      |             |
| Db                    | 75               | AGGCCCCCTCAAAGCGAGATCGCGCAGAGACTTGAAGATGCTTTGTGCGAGGAACAC        | 134      |             |
| Qy                    | 166              | CGAUUUGAGGUUCUAUGGAAUUGGCUAAAGACAAGACCAAUCCUGUCACCUUGACUAA       | 225      |             |
| Db                    | 135              | CGATCTTTGAGGCACATCGAATGGAAATGGCTAAAGACAAGACCAATCCTGTCACTCTGACTAA | 194      |             |
| Qy                    | 226              | GGGGAUUUAGGAUUUGUUCUACGUCACACGUGGCCAGUGAGCGAGGACUUGCAGCGUAG      | 285      |             |
| Db                    | 195              | AGGAAUATTTAGGATTCGTATTTACCGCTCACCGTCCCGAGTGAAGGAGACTGCACGGTAG    | 254      |             |
| Qy                    | 286              | ACGCUUUGUCCAAAUGCCUUAAUUGGAAACGGGGAUCCAAUAA CAUGGACAAAGCAGU      | 345      |             |
| Db                    | 255              | ACGCTTTGTCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGT     | 314      |             |
| Qy                    | 346              | UAAACUGUAUAGGAAGCUCAAGAGGGAUAUACAUIUCCAUUGGGGCCAAAGAAUUCUCACU    | 405      |             |
| Db                    | 315              | AAAACTGTACAGGAAGCTTAAAGAGAGAAATAACATTCATCGGGGCAAAAGGTTGGCAGT     | 374      |             |
| Qy                    | 406              | CAGUUAUUCUGCGUGGACUUCGCCAGUUAUUGGGCCUCAAUAUACAACAGGAUGGGGCG      | 465      |             |
| Db                    | 375              | CAGCTATTCACCTGGTGACCTAGCCACCTGCACTGGGAATCATATACACAGATATGGGAAC    | 434      |             |
| Qy                    | 466              | UGAGACCA CUGAAGUGGCAUUGGCGUGGUAUUGGCAACCUUGUGAACAGAUUUGUGACUVC   | 525      |             |
| Db                    | 435              | TGTGACAAACCGAAGTGGCATTTGGCTCTGATGCGCCACATGTGAAACAGATCGCTGATTC    | 494      |             |
| Qy                    | 526              | CCAGCAUGGUCUCAAUGGCAAAUUGGUGACAACAACCAACCA CUAUACAGACAUAGAA      | 585      |             |
| Db                    | 495              | CCAGCATCGATCTCA CAGGCAGATGGGTGACAAACCAACCCATTAATCAGACATGAAGA     | 554      |             |
| Qy                    | 586              | CAGAAUGGUUUUAGCCACCAUACAGCUAAGGCUAUGGAGCAAAUUGGUGGAUCCAGUGA      | 645      |             |
| Db                    | 555              | CAGAAUATGGTATTAGCCAGTACCA CGGCTTAAGCCATGGAGCGAGATGGCAGGGTCCAGTGA | 614      |             |
| Qy                    | 646              | GCAAGCAGCAGAGGCCAUUGGAGGUUUGUAGUCAGGCUAGGCAAAUUGGUGCAAGCAUGAG    | 705      |             |
| Db                    | 615              | GCAGGCAGCAGAGGCCATGGAGGTTTGCTAGTAAGGCTAGGCAGATGGTTCAGCAATGAG     | 674      |             |
| Qy                    | 706              | AACCAUUGGGA CUCUAUCCUAGCUCAGUGUCUGGUCUGUAAAUAUAGUAUUCUUAUUAUUU   | 765      |             |
| Db                    | 675              | AACATTTGGGACCAACCCATGCTCCAGTCCCGGTTTGAAGATGATCTCTTTGAAAAATTT     | 734      |             |









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Db 495 CCAGCATCGATCTCACAGGCAGATGGTGACATTAACCAACCCATTATACAGACATGAAA 554
Qy 586 CAGAAUGGUUUUAGCCAGCACUACAGCAGCUAAGGCUAGGCAAAUUGCUGGACUAGUGA 645
Db 555 CAGAAUGGUUUUAGCCAGCACUACAGCAGCUAAGGCUAGGCAAAUUGCUGGACUAGUGA 614
Qy 646 GCAAGCAGCAGAGGCGCAAGGAGGUUUGUAGUCAGGCUAGGCAAAUUGCUGGACUAGUGA 705
Db 615 GCAGGCAGCAGAGGCGCAAGGAGGUUUGUAGUCAGGCUAGGCAAAUUGCUGGACUAGUGA 674
Qy 706 AACCAUUGGACUACUACGUCAGGCUAGGCUAGGCAAAUUGCUGGACUAGUGA 765
Db 675 AACCAUUGGACUACUACGUCAGGCUAGGCUAGGCAAAUUGCUGGACUAGUGA 734
Qy 766 GCAGGCAGCAGAGGCGCAAGGAGGUUUGUAGUCAGGCUAGGCAAAUUGCUGGACUAGUGA 816
Db 735 GCAGGCAGCAGAGGCGCAAGGAGGUUUGUAGUCAGGCUAGGCAAAUUGCUGGACUAGUGA 785

RESULT 11
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: Education
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CL-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-434-811A-4

Query Match 68.4%; Score 644.6; DB 3; Length 1023;
Best Local Similarity 70.7%; Pred. No. 3.8e-145;
Matches 545; Conservative 147; Mismatches 79; Indels 0; Gaps 0;

Qy 46 AGAUUAAAGAGUAGUUCUUAACCGAGGUGGAAAGCUUUCUUCUUAUUAUUAUUAUUAUUA 105
Db 15 ATATTTAAGATGATCTTTCAGCGAGGTGAAACGATGCTTCTATCTTACCATC 74

Qy 106 AGGCCCCCUAAAGCGAGUAGCGCAGAGACUUAAGAGUAGUUCUUAUUAUUAUUAUUAUUA 165
Db 75 AGGCCCCCTCAAGCGAGATCGCGCAGAGACTTGAAGATGCTTTTGCAGGGAAGAACAC 134

Qy 166 CGAUUUGAGUUCUUAUUAAGGCUUAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 225
Db 135 CGATCTTGAGGCACTCATGTAAGTGGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194

Qy 226 GGGAGUUAUUAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 285
Db 195 AGGAGATTTAGATTCGATTTACGCTCACCGTCCCGAGTGAAGAGAGAGAGAGAGAGAGAG 254

Qy 286 ACGUUUUGUCCAAUUGCCUUUAUUGGAGAGCGGGAUCCAAUUAUUAUUAUUAUUAUUAUUA 345
Db 255 ACGCTTTGTCNAATGCGCTTAGTGGAAACGAGAGATCCAAACACATGGAGCAGAGCAGT 314

Qy 346 UAAACUUAUUAAGAGAGUUAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
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Db 315 AAAAATGTACAGAGAGCTTAAAGAGAGAAATAACATTCATGGGCAAAAGAGGTGGCACT 374
Qy 406 CAGUUAUUCUGCUGGUGCACAUCUCCAGUUGUUAUUGGCGCUCAUAUACAACAGGAUUGGGGC 465
Db 375 CAGCTATTCCACTGGTGTCACTAGCCAGCTGCTAGGGACTCATATACACAGAAATGGGAAC 434
Qy 466 UGUGACCAUUAAGUGGCAUUAUUGGCUUGUUAUUGGCAUUAUUGGCAUUAUUGGCAUUAU 525
Db 435 TGTGACAAACGAAAGTGGCATTTTGGCTGTGTATGCGCCACATGTGAAACAGATCGCTGATTC 494
Qy 526 CCAGCAUCGUCUUAUAGGCAAAUUGGCAUUAUUGGCAUUAUUGGCAUUAUUGGCAUUAUUG 585
Db 495 CCAGCATCGATCTCACAGGCAGATGGTGACATTAACCAACCCATTATACAGACATGAAA 554
Qy 586 CAGAAUGGUUUUAGCCAGCACUACAGCAGCUAAGGCUAGGCAAAUUGCUGGACUAGUGA 645
Db 555 CAGAAUGGUUUUAGCCAGCACUACAGCAGCUAAGGCUAGGCAAAUUGCUGGACUAGUGA 614
Qy 646 GCAAGCAGCAGAGGCGCAAGGAGGUUUGUAGUCAGGCUAGGCAAAUUGCUGGACUAGUGA 705
Db 615 GCAGGCAGCAGAGGCGCAAGGAGGUUUGUAGUCAGGCUAGGCAAAUUGCUGGACUAGUGA 674
Qy 706 AACCAUUGGACUACUACGUCAGGCUAGGCUAGGCAAAUUGCUGGACUAGUGA 765
Db 675 AACCAUUGGACUACUACGUCAGGCUAGGCUAGGCAAAUUGCUGGACUAGUGA 734
Qy 766 GCAGGCAGCAGAGGCGCAAGGAGGUUUGUAGUCAGGCUAGGCAAAUUGCUGGACUAGUGA 816
Db 735 GCAGGCAGCAGAGGCGCAAGGAGGUUUGUAGUCAGGCUAGGCAAAUUGCUGGACUAGUGA 785

RESULT 12
US-09-506-286B-3
; Sequence 3, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-3

Query Match 67.6%; Score 637.2; DB 3; Length 756;
Best Local Similarity 71.0%; Pred. No. 2.1e-143;
Matches 537; Conservative 145; Mismatches 74; Indels 0; Gaps 0;

Qy 56 AUGAGUUCUUAACCGAGGUGGAAACGUAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUA 115
Db 1 ATGAGTCTTCTGACCGAGGTGGAACGATGCTTCTATCTGTACCATCAGGCCCCCTC 60

Qy 116 AAAGCCCGAGAUCCGACAGAGACUUAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 175
Db 61 AAAGCCCGAGATCGGACAGAGACTTGAAGATGCTTTTCAGGGAAGAACACCGATCTTGAG 120

Qy 176 GUUCUUAUUAAGGCUUAUUAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 235
Db 121 GCATCATGAATGGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

Qy 236 GGAUUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 295
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Db 181 GGAATCGTATTACCGCTCACCGTGCAGAGGAGTGCAGCGTAGACGCTTTGTC 240  
Qy 296 CAAAUAUCCUUAUAGCGGGAUCCAAUAUACUAGGCAAGCAGUUAACUGU 355  
Db 241 CAAATGCGCTTAGTGGAAACGGAGATCAAACACATGGAAGAGTAAAGTGTAC 300  
Qy 356 AGGAGCUCUAGAGGAGGAUACAUUCCAUUGGGCCAAAGAAUUCUCACUAGUUAUUCU 415  
Db 301 AGGAGCTTAAAGAGAAATTAACATTCCATGGGGCAAAAGAGTGGCACTCAGCTATTCC 360  
Qy 416 GCUGUGCUCUUGCCAGUUAUUGGCGCCUUAUAUACAAACAGAGUUGGGGUGUGACCAU 475  
Db 361 ACTGCTGCACTAGCCAGCTGCACTGGAATCTATATACAGAAATGGGAATGTGACCAAC 420  
Qy 476 GAAUGGCAUUGGCGUUAUGGCAACUUGGCAACAGUUAUUGGCAUUGGCAUUGG 535  
Db 421 GAAGTGGCATTTGGCTGGTATGCGCCACATGTGAACAGATGCGTGTATCCAGCATCGA 480  
Qy 536 UCUAUAGGCAAAUGGUGACAAACCAACCAACCAUUAUCAGACAUAGAAACAGAAUGGU 595  
Db 481 TCTCAGCGAGATGCTGACACCAACCAACCAATTAATCAGACATGAACAGAAATGGTA 540  
Qy 596 UUAGCCAGCACAUAAGCUGUAUGGCAUAGGCAUAGGCAUAGGCAUAGGCAUAGGCA 655  
Db 541 TTAGCCAGTACCAAGGCTAAAGCCATGAGCAGATGGCAGGCTCGAGTGAGCAGCAGCA 600  
Qy 656 GAGGCAUAGGAGUUGUAGUAGGCAUAGGCAUAGGCAUAGGCAUAGGCAUAGGCA 715  
Db 601 GAGGCAUAGGAGUUGUAGUAGGCAUAGGCAUAGGCAUAGGCAUAGGCAUAGGCA 660  
Qy 716 ACUAUAGGAGUUGUAGUAGGCAUAGGCAUAGGCAUAGGCAUAGGCAUAGGCA 775  
Db 661 ACCACCTAGCTCAGTCCGCTTTGAAAGATGATCTCTTGAATTTGAGGCTTAC 720  
Qy 776 CAGAAACGAUUGGCGGUGCAGUAGCAACCGUUAAG 811  
Db 721 CAGAAACGGATGGAGTGCAAAATGCGAGGATTCAAG 756

## RESULT 13

US-09-762-861B-3  
; Sequence 3, Application US/09762861B  
; Patent No. 6579528  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)  
; CURRENT APPLICATION NUMBER: US/09/762,861B  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-09-762-861B-3

Query Match 67.6%; Score 637.2; DB 3; Length 756;  
Best Local Similarity 71.0%; Pred. No. 2.1e-143;  
Matches 537; Conservative 145; Mismatches 74; Indels 0; Gaps 0;

Qy 56 AUGAGUUCUUAACCGAGGUGCAAGUAGUUCUUAUAGGCAUAGGCAUAGGCAUAGGCA 115  
Db 1 ATGAGTCTTCTGACCGAGGTGCAAAACGTAAGTCTCTATCGTACCATCATGAGGCCCCCTC 60

Qy 116 AAAGCCGAGUAGCGCAGACAGACUUGAAGAUUGUUCUUGCAGGGGAAGAACACCGAUUCUGAG 175  
Db 61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGACGGAAGAAACACCGATCTTGAG 120  
Qy 176 GUUCUCAUGAUAUGGCUAAAGACAGACCAUCCUGUACCUUGUACCUUGUACCUUGUACCU 235  
Db 121 GCACTCATGAATGGCTAAAGACAAGACCAATCTGTCTGACTTAAGGGATTTTA 180  
Qy 236 GGAUUGUGUUCACGUCACCGUCCAGUGAGGAGGAGCUGCAGCGUAGACGCUUUGUC 295  
Db 181 GGATTCGTATTACGCTCA CGGTGCCAGTGAGCGGAGGACTGCGAGCGTGAAGCGTTGTC 240  
Qy 296 CAAAAGCCUUAUAGGGAACCGGGAUCCAAAUAUACAGGCAAAAGCAGUUAACUGU 355  
Db 241 CAAAATGCCCTTAGTGGAAACGGAGATCCAAAACAATGAGCAGAGCAGTAAAGCTGATC 300  
Qy 356 AGGAGCUCUAGAGGAGGAUUAUUCUUGGCGCCAAAGAAUUCUACUACUAGUUAUUCU 415  
Db 301 AGGAAGCTTAAAGAGAAATAACAATTCATGGGGCAAAAGAGTGGCACTCAGCTATTCC 360  
Qy 416 GCUGGCAUUGGCAUUGGCGCUUAUAGGCGCUUAUUAUACAAAGAGGCGGUGUGACCAU 475  
Db 361 ACTGCTGCACTAGCCAGCTGCTGGAATCATATACAGAGATGGGAATCTGTGACCAAC 420  
Qy 476 GAAUGGCAUUGGCGCUUGUAGGCAUAGGCAUAGGCAUAGGCAUAGGCAUAGGCA 535  
Db 421 GAAGTGGCATTTGGCTGGTATGCGCCACATGTGAACAGATCGCTGATTCCAGCATCGA 480  
Qy 536 UCUAUAGGCAAAUGGUGACAAACCAACCAACCAUUAUCAGACAUAGAAACAGAAUGGU 595  
Db 481 TCTCAGAGGAGATGCTGACACCAACCAACCAATTAATCAGACATGAACAGAAATGGTA 540  
Qy 596 UUAAGCAGCACAUAAGGCGUUAUGGCAUAGGCAUAGGCAUAGGCAUAGGCAUAGGCA 655  
Db 541 TTAGCCAGTACCAAGGCTAAAGCCATGAGCAGATGGCAGGCTCGAGTGAGCAGCAGCA 600  
Qy 656 GAGGCAUAGGAGUUGUAGUAGGCAUAGGCAUAGGCAUAGGCAUAGGCAUAGGCA 715  
Db 601 GAGGCAUAGGAGUUGUAGUAGGCAUAGGCAUAGGCAUAGGCAUAGGCAUAGGCA 660  
Qy 716 ACUAUAGGAGUUGUAGUAGGCAUAGGCAUAGGCAUAGGCAUAGGCAUAGGCAUAGGCA 775  
Db 661 ACCACCTAGCTCAGTCCGCTTTGAAAGATGATCTCTTGAATTTGAGGCTTAC 720  
Qy 776 CAGAAACGAUUGGCGGUGCAGUAGCAACCGUUAAG 811  
Db 721 CAGAAACGGATGGAGTGCAAAATGCGAGGATTCAAG 756

## RESULT 14

US-10-065-133A-3  
; Sequence 3, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-3

Query Match 67.6%; Score 637.2; DB 3; Length 756;



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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:29:50 ; Search time 925.936 Seconds  
(without alignments)  
8412.838 Million cell updates/sec

Title: US-10-729-830-5

Perfect score: 942

Sequence: 1 gcugucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaaa 942

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

#### Database :

Published Applications NA Main:  
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3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
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9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Query | Score | Match | Length | DB               | ID | Description       |
|------------|-------|-------|-------|--------|------------------|----|-------------------|
| 1          | 942   | 100.0 | 942   | 8      | US-10-729-830-5  |    | Sequence 5, Appli |
| 2          | 774   | 82.2  | 774   | 8      | US-10-729-830-1  |    | Sequence 1, Appli |
| 3          | 764.6 | 81.2  | 1027  | 6      | US-10-177-390-31 |    | Sequence 31, Appl |
| 4          | 761.4 | 80.8  | 1027  | 6      | US-10-855-875-5  |    | Sequence 5, Appli |
| 5          | 718.2 | 76.2  | 1027  | 7      | US-10-381-530-7  |    | Sequence 7, Appli |
| 6          | 666.8 | 70.8  | 942   | 8      | US-10-729-830-6  |    | Sequence 6, Appli |
| 7          | 655.4 | 69.6  | 986   | 8      | US-10-866-484-9  |    | Sequence 9, Appli |
| 8          | 647.4 | 68.7  | 1023  | 6      | US-10-065-133A-1 |    | Sequence 1, Appli |
| 9          | 647.4 | 68.7  | 1023  | 6      | US-10-434-811A-1 |    | Sequence 1, Appli |
| 10         | 647.4 | 68.7  | 1023  | 7      | US-10-734-373-1  |    | Sequence 1, Appli |
| 11         | 647.4 | 68.7  | 1023  | 8      | US-10-872-014-1  |    | Sequence 1, Appli |
| 12         | 645.8 | 68.6  | 1002  | 3      | US-09-747-335-3  |    | Sequence 3, Appli |
| 13         | 645.8 | 68.6  | 1002  | 7      | US-10-435-723A-3 |    | Sequence 3, Appli |
| 14         | 644.6 | 68.4  | 1023  | 6      | US-10-065-133A-4 |    | Sequence 4, Appli |
| 15         | 644.6 | 68.4  | 1023  | 7      | US-10-434-811A-4 |    | Sequence 4, Appli |
| 16         | 644.6 | 68.4  | 1023  | 7      | US-10-734-373-4  |    | Sequence 4, Appli |
| 17         | 644.6 | 68.4  | 1023  | 8      | US-10-872-014-4  |    | Sequence 4, Appli |
| 18         | 637.2 | 67.6  | 756   | 6      | US-10-065-133A-3 |    | Sequence 3, Appli |
| 19         | 637.2 | 67.6  | 756   | 7      | US-10-434-811A-3 |    | Sequence 3, Appli |
| 20         | 637.2 | 67.6  | 756   | 7      | US-10-734-373-3  |    | Sequence 3, Appli |
| 21         | 637.2 | 67.6  | 756   | 8      | US-10-872-014-3  |    | Sequence 3, Appli |
| 22         | 634.4 | 67.3  | 756   | 6      | US-10-065-133A-6 |    | Sequence 6, Appli |
| 23         | 634.4 | 67.3  | 756   | 7      | US-10-434-811A-6 |    | Sequence 6, Appli |

|    |       |      |      |   |                      |                   |
|----|-------|------|------|---|----------------------|-------------------|
| 24 | 634.4 | 67.3 | 756  | 7 | US-10-734-373-6      | Sequence 6, Appli |
| 25 | 634.4 | 67.3 | 756  | 8 | US-10-872-014-6      | Sequence 6, Appli |
| 26 | 632.6 | 67.2 | 816  | 6 | US-10-371-525-13     | Sequence 13, Appl |
| 27 | 632.6 | 67.2 | 816  | 6 | US-10-371-069-13     | Sequence 13, Appl |
| 28 | 632.6 | 67.2 | 816  | 6 | US-10-371-645-13     | Sequence 13, Appl |
| 29 | 632.6 | 67.2 | 816  | 6 | US-10-371-260-13     | Sequence 13, Appl |
| 30 | 627.8 | 66.6 | 759  | 8 | US-10-617-569-3      | Sequence 3, Appli |
| 31 | 608.8 | 64.6 | 1011 | 8 | US-10-729-830-7      | Sequence 7, Appli |
| 32 | 499.8 | 53.1 | 775  | 8 | US-10-729-830-3      | Sequence 3, Appli |
| 33 | 486.8 | 51.7 | 844  | 8 | US-10-729-830-4      | Sequence 4, Appli |
| 34 | 99.6  | 10.6 | 132  | 3 | US-09-835-694-54     | Sequence 54, Appl |
| 35 | 96.6  | 10.3 | 129  | 3 | US-09-835-694-55     | Sequence 55, Appl |
| 36 | 87.4  | 9.3  | 122  | 3 | US-09-835-694-17     | Sequence 17, Appl |
| 37 | 84.2  | 8.9  | 573  | 7 | US-10-424-599-135848 | Sequence 135848,  |
| 38 | 83.4  | 8.9  | 362  | 8 | US-10-425-115-68338  | Sequence 68338, A |
| 39 | 83    | 8.8  | 598  | 7 | US-10-021-323-11423  | Sequence 11423, A |
| 40 | 82.8  | 8.8  | 510  | 7 | US-10-437-963-1928   | Sequence 1928, Ap |
| 41 | 82.6  | 8.8  | 374  | 7 | US-10-437-963-32121  | Sequence 32121, A |
| 42 | 82    | 8.7  | 405  | 8 | US-10-425-115-76344  | Sequence 76344, A |
| 43 | 82    | 8.7  | 1714 | 8 | US-10-425-115-170894 | Sequence 170894,  |
| 44 | 81.6  | 8.7  | 554  | 7 | US-10-021-323-4489   | Sequence 4489, Ap |
| 45 | 81.6  | 8.7  | 559  | 7 | US-10-021-323-14094  | Sequence 14094, A |

#### ALIGNMENTS

##### RESULT 1

US-10-729-830-5  
; Sequence 5, Application US/10729830  
; Publication No. US20050032730A1  
; GENERAL INFORMATION:  
; APPLICANT: Von der Muelbe, Florian  
; APPLICANT: Hoerr, Ingrid  
; APPLICANT: Pascolo, Steve  
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA  
; FILE REFERENCE: 2793-1-001PCT/CIP  
; CURRENT APPLICATION NUMBER: US/10/729,830  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: PCT/BP02/06180  
; PRIOR FILING DATE: 2002-06-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 942  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Influenza  
; OTHER INFORMATION: matrix: mRNA with stabilisation sequences  
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-  
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,  
; OTHER INFORMATION: respectively.  
; FEATURE:  
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop  
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)  
US-10-729-830-5

Query Match 100.0%; Score 942; DB 8; Length 942;  
Best Local Similarity 100.0%; Pred. No. 1.8e+220;  
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCUGUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAUUAUCCCGCAGGCCCCCUCAAGC 60  
Db 1 GCUGUCUUUUUGCAGAAGCUCAGAAUAAACGCUCAUUAUCCCGCAGGCCCCCUCAAGC 60  
Qy 61 UCUUUAACCGAGGUCGAAACGUAUUCUUAUUAUCCCGCAGGCCCCCUCAAGC 120  
Db 61 UCUUUAACCGAGGUCGAAACGUAUUCUUAUUAUCCCGCAGGCCCCCUCAAGC 120  
Qy 121 CGAGUUCGACAGACUUGAAGUUGUUCAGGGAAGAACACCGAUUCUUGAGGUUCU 180

Db 121 CGAUCGCGCAGAGACUUGAAGAUUGUUUGCAGGAGAACACCGAUUUUGAGGUUCU 180  
Qy 181 CAUGGAUUGGUAAGGCAAGACCAUCCUGUCACCUUGUCAGCUAAGGGGUAUUUAGGAUU 240  
Db 181 CAUGGAUUGGUAAGGCAAGACCAUCCUGUCACCUUGUCAGCUAAGGGGUAUUUAGGAUU 240  
Qy 241 UGUUUUACGUCACCGUGGCCAGUGAGCGAGGAGGACUGCAGGCUAGAGCGUUUGUCCAAAA 300  
Db 241 UGUUUUACGUCACCGUGGCCAGUGAGCGAGGAGGACUGCAGGCUAGAGCGUUUGUCCAAAA 300  
Qy 301 UGCCUUUAUUGGGACCGGGAUCCAAUAUAUCGACCAAAACAGUAUUAUAGGAA 360  
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Db 361 GCUCAAGAGGAGAGAAUUAUCCAUUGGGGCCAAAGAAUUCACUCAGUAUUAUUCUGUG 420  
Qy 421 UGCAUUGCCAGUUGUAUUGGGCCUUAUAUAACAAGGAGUGGGGCGUGUACCAUGAAGU 480  
Db 421 UGCAUUGCCAGUUGUAUUGGGCCUUAUAUAACAAGGAGUGGGGCGUGUACCAUGAAGU 480  
Qy 481 GGCATUUGCCUGUUAUGCAACUUGUAACAGAUUGCUCAUCCAGCAUCCGUCUCA 540  
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Qy 781 ACAGUUGGGGUGCAGUAGCAACCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840  
Db 781 ACAGUUGGGGUGCAGUAGCAACCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840  
Qy 841 CUCCCAAGCGGCGUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCC 900  
Db 841 CUCCCAAGCGGCGUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCC 900  
Qy 901 AA 942  
Db 901 AA 942

RESULT 2  
US-10-729-830-1  
; Sequence 1, Application US/10729830  
; Publication No. US20050032730A1  
; GENERAL INFORMATION:  
; APPLICANT: Von der Muelbe, Florian  
; APPLICANT: Hoerr, Ingmar  
; APPLICANT: Pascolo, Steve  
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA  
; FILE REFERENCE: 2793-1-001PCT/CIP  
; CURRENT APPLICATION NUMBER: US/10/729,830  
; PRIOR FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: PCT/EP02/06180  
; PRIOR FILING DATE: 2002-06-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1  
; LENGTH: 774  
; TYPE: DNA  
; ORGANISM: Influenza virus  
; FEATURE:  
; OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)  
; FEATURE:  
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop  
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)  
US-10-729-830-1  
  
Query Match 82.2%; Score 774; DB 8; Length 774;  
Best Local Similarity 77.6%; Pred. No. 2.4e-179;  
Matches 601; Conservative 173; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 46 AGAUCUUAAGAGUAGUUCUUAACCCAGGUCGAAACGUAUUCUUCUUAUUAUUAUUAUUA 105  
Db 1 AGATCTAAAGATGAGTCTTCTAAACCGAGGTCGAAACGTCAGTCTCTCTATCATCCCGTC 60  
  
Qy 106 AGSCCCCUCAAAGCCGAGUACGACAGACAUUGAAGAUUGUUUGCAGGAGAAACAC 165  
Db 61 AGSCCCCTCAAAGCCGAGATCGACAGACTTTGAAGATGTCTTTGACGGGAGAAACAC 120  
  
Qy 166 CGAUUCUAGGUCUUAUGGAUUGGCUAAAGACAAGACCAUUCUGUCACCUUCUGACUUA 225  
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Qy 226 GGGGAUUUAAGGAUUUGUUCACGUCACCGUGCCGAGUGCGAGGAUGCAGCGUAG 285  
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Db 361 CAGTTATCTGCTGGTGCACTTGCCAGTTGTATGGGCTCATATATACACAGGATGGGGGC 420  
  
Qy 466 UGUGACCAUUAAGGUAUUGCCUUGUAUUGGUAUUGGUAUUGGUAUUGGUAUUGGUAUUG 525  
Db 421 TGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAAACAGATTGTCTGACT 480  
  
Qy 526 CCAGUACGUGUCUAUAGGCAAAUUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 585  
Db 481 CCAGCATCGGTCTCATAGGCAAAATGGTGAACAACCAACCAACCACTAATCAGACATGAA 540  
  
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Db 661 AACCATTTGGGACTCATCTCTAGCTCCAGTGTGGTCTGAAAAATGATCTCTTTGAAAAAT 720  
  
Qy 766 GCAGGCUUAUUAAGAAACAAUUGGGGUGCAGUAGCAACCGGUUAUUAUUAUUAUUAUUA 819  
Db 721 GCAGGCUATATCAGAAACGAATGGGGTGCAGATGCAACCGGTTCAAGTGAACATAG 774

RESULT 3  
US-10-177-390-31  
; Sequence 31, Application US/10177390  
; Publication No. US20030143743A1  
; GENERAL INFORMATION:















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Db 75 AGGCCCCCTCAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTGAGGGGAAGAACAC 134
Qy 166 CGAUUUGAGGUUCUACAUGGAUUGGCUAAAGACAAGACCAAUUCUGUCACCUUGACUAA 225
Db 135 CGATCTTGAAGCACTCATGGAATGGCTAAAGACAAGCAACCAATCTGTCAACCTCTGACTAA 194
Qy 226 GGGGAUUUAGGAUUUGUUGUUCACGUCUACCGUGCCAGUGAGCGAGGACUGGACGCUAG 285
Db 195 AGGGATTTTAGGATTCGTATTACGCTCACCGCTCCAGTCGCGAGTGGAGGAGACTGCGACGTAG 254
Qy 286 AGCUUUGUCCAAAUUGCCUUAUUGGGAUGGGAUGGAGGAGGAGGAGGAGGAGGAGGAGGAG 345
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Qy 346 UAAACUGUAUAGGAAGCUACAAGAGGAGAGUAUACAUCUUGGGGCCCAAGAAUUCUACU 405
Db 315 AAAACTGTACAGGAAGCTTAAAGAGAAATTAACATTCCATGGGGCAAAAGAGGTGGCACT 374
Qy 406 CAGUUUUCUGUCUGUGUUCUUGGAGUUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 465
Db 375 CAGCTATTCCACTGGTCACTAGCCAGCTGATGGGACTCATATACAAACAGAAATGGGAAC 434
Qy 466 UGUGACACUAGAUGGCAUUGGCUUGGUAUGGCAACUUGGUAAGAGGAGGAGGAGGAGGAG 525
Db 435 TGTGACAAACGGAATGGGCAATTTGGCTGGTATGGCCACATGTGAACAGATCGCTGATTC 494
Qy 526 CCAGCAGCGGUCUCAUAGGCAAAUUGGAGCAACCAACCAACCAUUAUUCAGACAUAGAA 585
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Qy 586 CAGAAUGUUUAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUUGGUGAGUAGGAGGAG 645
Db 555 CAGAATGGTATTAGCCAGTACCAAGCTTAAGCCATGGAGCAGATGGCAGGCTCGAGTGA 614
Qy 646 GCACGACGACAGGCGCAUUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 705
Db 615 GCAGGACGACAGAGGCCATGGAGGTTGCTAGTAGGCTAGGAGGAGGAGGAGGAGGAGGAG 674
Qy 706 AACCAUUGGGACUACUACGUCUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 765
Db 675 AACCATTTGGGACCCACCTAGCTCCAGTGCCGGTTTGAAGATGATCTCTCTTGAAGATTT 734
Qy 766 GCAGGCUUACAGAAACGAAUUGGGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 816
Db 735 GCAGGCGCTACCAAGAAACGAGTGGGAGTGCAAAATGCAGCGATTCAGATGATC 785
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## RESULT 12

US-09-747-335-3

; Sequence 3, Application US/09747335

; Patent No. US20020095692A1

; GENERAL INFORMATION:

; APPLICANT: Thomas, David

; APPLICANT: Skinner, Anita

; APPLICANT: Hay, Alan

; TITLE OF INVENTION: Conditional Mutants of Influenza Virus M2 Protein

; FILE REFERENCE: 18396/1500

; CURRENT APPLICATION NUMBER: US/09/747,335

; CURRENT FILING DATE: 2000-12-21

; PRIOR APPLICATION NUMBER: PCT/GB99/02204

; PRIOR FILING DATE: 1999-07-09

; PRIOR FILING DATE: 1998-07-10

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 1002

; TYPE: DNA

; ORGANISM: Influenza A virus

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(26)

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; OTHER INFORMATION: Exon
; NAME/KEY: misc feature
; LOCATION: (715)..(982)
; OTHER INFORMATION: Exon
US-09-747-335-3
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Query Match 68.6%; Score 645.8; DB 3; Length 1002;

Best Local Similarity 69.3%; Pred. No. 6.9e-148; Indels 0; Gaps 0;  
Matches 533; Conservative 159; Mismatches 77;

Qy 56 AUGAGUCUUCUAAACCCGAGGUCGAAAGUAAGUUCUUCUUAUACUCCGUCAGGCCCCUC 115

Db 1 ATGAGTCTTCTAACCAGGTTGAAACGTAAGTCTCTATCATCATCCATCAGGCCCTC 60

Qy 116 AAAGCCGAGAUCCGACAGAGACUUGAAGUUCUUGCAGGGAAGAACCCGUAUCUUGAG 175

Db 61 AAAGCCGAGATCGCGAGAGACTTGAAGATGTCTTTCAGGGGAAAAACACAGACCTTGAG 120

Qy 176 GUUCUUAUGGAUUGGCUAAAGACAAGACCAUUCUCCUCCUUCUUAAGGGGAUUUA 235

Db 121 GTTCTCATGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAAGGATTTTG 180

Qy 236 GGAUUUGUUCACGUCACCGUGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 295

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Db 361 ACTGGAGCACTTGCCAGTTGTATGGGCTCATATACACAGAACTGTGACCACA 420

Qy 476 GAAGUGCAUUUGGCCUUGUUAUGGCAACCGUGAACAAGUUGUAGUUGUUGUUGUUGUUG 535

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## RESULT 13

US-10-435-723A-3

; Sequence 3, Application US/10435723A

; Publication No. US20040055024A1

; GENERAL INFORMATION:

; APPLICANT: Thomas, David B

; APPLICANT: Skinner, Anita

; APPLICANT: Hay, Alan J

; TITLE OF INVENTION: Conditional Mutants of Influenza Virus M2 Protein

; FILE REFERENCE: 18396/1503





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Qy 766 GCAGGCCTACAGAAACCGAAGGCGGUGCAGAGCUAGGCUAGGCUAGGCUAGGCUA 816
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RESULT 15
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; Education
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CL-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-434-811A-4

Query Match 68.4%; Score 644.6; DB 7; Length 1023;
Best Local Similarity 70.7%; Pred. No. 1.4e-147;
Matches 545; Conservative 147; Mismatches 79; Indels 0; Gaps 0;

Qy 46 AGAUUAAAGAUAGAGUCUUAACCGAGGUGGAAACGUACGUUCUCUUAUUAUCCCGUC 105
Db 15 ATATTAAAGATGATGCTTCTGACCGAGTGGAAACGATACCTCTCTATCTTACCATC 74

Qy 106 AGGCCCCUCUAAAGCCGAGUUCGACAGAGACUUAAGUAGUUCUUGCAGGGAAGAACAC 165
Db 75 AGGCCCCCTCAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTGCGAGGGAAGAACAC 134

Qy 166 CGAUUCUAGGUCUUAUGGAAUUGGCUAAGCAAGCAACUCCUUGUACCUUGAGCUAA 225
Db 135 CGATCTTGAGGCACTCATGGAATGGCTAAAGCAAGCAACATCTGTCTCCTCTGACTAA 194

Qy 226 GGGGAAUUAAGAUUUGUUCACGCUACGUGCCAGUGAGCGAGGAGGAGGAGGAGGAGG 285
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Qy 286 ACGUUGUUCUAAAGCCUUAUUGGAAACGGGGAUCCAAAUAAUAGGACAAAGCAGU 345
Db 255 ACGCTTTGTCAAAATGCGCTTAGTGGAAACGGAGATCCAAACAAACATGGACAGAGCAGT 314

Qy 346 UAAACUGUUAAGGAGCUAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 405
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Qy 466 UGUGACCAUUGAAGUGGCUUUGGCGGCUUUGGCUUUGGCUUUGGCUUUGGCUUUGGCU 525
Db 435 TGTGACAAACCGAAGTGGCATTTGGCTGTGTATGGCCACATGTGAAACAGATCGCTGATTC 494
Qy 526 CCAGCAUUGGCUUUAUAGGCAAAUUGGUGACAAACCAACCAACCAUUAUUAUUAUUAUUA 585
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Db 675 AACCAUUGGACUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUA 734
Qy 766 GCAGGCCTACAGAAACCGAAGGCGGUGCAGAGCUAGGCUAGGCUAGGCUAGGCUA 816
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GenCore version 5.1.7  
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Searched: 8023312 seqs, 1165852854 residues

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Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB\_seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Score | Length | DB ID | Description                          |
|------------|-------------|-------|--------|-------|--------------------------------------|
| 1          | 758.2       | 80.5  | 1027   | 12    | US-11-131-479-3 Sequence 3, Appli    |
| 2          | 749.6       | 79.6  | 1305   | 12    | US-11-131-479-45 Sequence 59, Appl   |
| 3          | 700.2       | 74.3  | 987    | 12    | US-11-155-478A-131 Sequence 131, App |
| 4          | 689.4       | 73.2  | 1027   | 12    | US-11-155-478A-130 Sequence 130, App |
| 5          | 681.6       | 72.4  | 4822   | 12    | US-11-131-479-95 Sequence 95, Appl   |
| 6          | 681.6       | 72.4  | 7798   | 12    | US-11-131-479-97 Sequence 97, Appl   |
| 7          | 681.6       | 72.3  | 982    | 12    | US-11-131-479-98 Sequence 98, Appl   |
| 8          | 681         | 72.3  | 982    | 12    | US-11-131-479-60 Sequence 60, Appl   |
| 9          | 681         | 72.3  | 5161   | 12    | US-11-131-479-101 Sequence 101, App  |
| 10         | 681         | 72.3  | 5398   | 12    | US-11-131-479-91 Sequence 91, Appl   |
| 11         | 681         | 72.3  | 7798   | 12    | US-11-131-479-99 Sequence 99, Appl   |
| 12         | 681         | 72.3  | 7798   | 12    | US-11-131-479-100 Sequence 100, App  |
| 13         | 681         | 72.3  | 8442   | 12    | US-11-131-479-106 Sequence 106, App  |
| 14         | 681         | 72.3  | 8442   | 12    | US-11-131-479-107 Sequence 107, App  |
| 15         | 681         | 72.3  | 8450   | 12    | US-11-131-479-104 Sequence 104, App  |
| 16         | 681         | 72.3  | 8450   | 12    | US-11-131-479-105 Sequence 105, App  |
| 17         | 526.6       | 55.9  | 629    | 9     | US-11-137-807-18 Sequence 18, Appl   |
| 18         | 502         | 53.3  | 982    | 12    | US-11-131-479-61 Sequence 61, Appl   |
| 19         | 501.4       | 53.2  | 759    | 12    | US-11-131-479-79 Sequence 79, Appl   |
| 20         | 474.4       | 50.4  | 756    | 12    | US-11-131-479-27 Sequence 27, Appl   |

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|----|-------|------|------|----|---------------------|-------------------|
| 21 | 471.2 | 50.0 | 756  | 12 | US-11-131-479-28    | Sequence 28, Appl |
| 22 | 464   | 49.3 | 1050 | 12 | US-11-131-479-59    | Sequence 59, Appl |
| 23 | 459.8 | 48.8 | 759  | 12 | US-11-131-479-69    | Sequence 69, Appl |
| 24 | 447.8 | 47.5 | 756  | 12 | US-11-131-479-26    | Sequence 26, Appl |
| 25 | 477.4 | 8.2  | 1180 | 12 | US-11-116-746-2     | Sequence 2, Appli |
| 26 | 77.4  | 8.2  | 1180 | 12 | US-11-116-746-4     | Sequence 4, Appli |
| 27 | 75.8  | 8.0  | 588  | 12 | US-11-136-527-1488  | Sequence 1488, Ap |
| 28 | 75.8  | 8.0  | 588  | 12 | US-11-136-527-5584  | Sequence 5584, Ap |
| 29 | 75.2  | 8.0  | 1677 | 7  | US-10-515-547-3     | Sequence 3, Appli |
| 30 | 75.2  | 8.0  | 4339 | 8  | US-10-909-125-801   | Sequence 801, App |
| 31 | 74.8  | 7.9  | 2475 | 9  | US-11-197-133A-17   | Sequence 17, Appl |
| 32 | 74.8  | 7.9  | 5152 | 8  | US-10-240-708-47    | Sequence 47, Appl |
| 33 | 74.6  | 7.9  | 1395 | 8  | US-10-955-054A-111  | Sequence 111, App |
| 34 | 74.6  | 7.9  | 2217 | 8  | US-10-947-249-197   | Sequence 197, App |
| 35 | 74.6  | 7.9  | 3819 | 7  | US-10-973-115B-405  | Sequence 405, App |
| 36 | 74.6  | 7.9  | 3819 | 8  | US-10-131-826A-405  | Sequence 405, App |
| 37 | 74.4  | 7.9  | 600  | 12 | US-11-136-527-6371  | Sequence 6371, Ap |
| 38 | 74.4  | 7.9  | 2020 | 12 | US-11-090-617-697   | Sequence 697, App |
| 39 | 74.4  | 7.9  | 3015 | 12 | US-11-183-136-39    | Sequence 39, Appl |
| 40 | 74.4  | 7.9  | 4409 | 12 | US-11-136-527-2275  | Sequence 2275, Ap |
| 41 | 74.2  | 7.9  | 1905 | 8  | US-10-947-249-132   | Sequence 132, App |
| 42 | 74    | 7.9  | 1690 | 12 | US-11-090-439-43    | Sequence 43, Appl |
| 43 | 73.8  | 7.8  | 588  | 8  | US-10-689-742-41    | Sequence 41, Appl |
| 44 | 73.6  | 7.8  | 762  | 9  | US-11-096-568A-1243 | Sequence 1243, A  |
| 45 | 73.6  | 7.8  | 2845 | 7  | US-10-973-115B-207  | Sequence 207, App |

ALIGNMENTS

RESULT 1

US-11-131-479-3

; Sequence 3, Application US/11131479

; Publication No. US20060024670A1

; GENERAL INFORMATION:

; APPLICANT: Luke, Catherine J.

; APPLICANT: Vilalta, Adrian

; APPLICANT: Wloch, Mary K.

; APPLICANT: Evans, Thomas G.

; APPLICANT: Geall, Andrew J.

; APPLICANT: Jimenez, Gretchen

; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use

; FILE REFERENCE: 1530.0640002/EJH/J-H

; CURRENT APPLICATION NUMBER: US/11/131,479

; CURRENT FILING DATE: 2005-05-18

; PRIOR APPLICATION NUMBER: US 60/571,854

; PRIOR FILING DATE: 2004-05-18

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 3

; LENGTH: 1027

; TYPE: DNA

; ORGANISM: Influenza A virus

US-11-131-479-3

|                       |       |  |        |                |
|-----------------------|-------|--|--------|----------------|
| Query Match           | 80.5% | Score 758.2;   | DB 12; | Length 1027;   |
| Best Local Similarity | 76.3% | Pred. No. 2.4e-84;   |        |                |
| Matches               | 594;  | Conservative   | 172;   | Mismatches 13; |
| Indels                | 0;    | Gaps   | 0;     |                |
| Qy                    | 46    | AGAUCAAAGAUGAGUCUUAACCGAGGUGCGAAACGUAACGUCUCUUAUCCCGUC     | 105    |                |
| Db                    | 16    | ATATTGAAGATGAGTCTTCTACCGAGGTCGAAACGCTACTCTCTATCATCCGTC     | 75     |                |
| Qy                    | 106   | AGGCCCCCUCAAGCCAGACGACAGACUUAAGAGUUCUUAUCCGAGGAGAACAC      | 165    |                |
| Db                    | 76    | AGGCCCCCTCAAAGCCGAGATCGCACAGAGATGTCTTTCAGGGAGAGACAC        | 135    |                |
| Qy                    | 166   | CGAUCUUGAGUUCUUAAGGCUAAAGACAAAGACACCAUCCUCCUACCUACUAA      | 225    |                |
| Db                    | 136   | TGATCTTGAGGTCTCTATGAATGGCTAAAGACAAAGACCAATCTGTCACTCTGACTTA | 195    |                |
| Qy                    | 226   | GGGGAUUAUAGGAUUGUGUUCACGUCACCGUGCCAGAGGAGGAGGAGGAGCGUAG    | 285    |                |

Db 196 GGGGATTTTAGGATTTGTGTTCA CGCTCA CCGTCCCGCAGTGAGCGAGACTGCGAGCGTAG 255  
Qy 286 ACGCUUUGUCCAAAUUGCCCUUAAUUGGGAACGGGGAUCCAAUUAACAUUGGACAAAGCAGU 345  
Db 256 ACGCTTTGTCCTAAATGCCCTTAATGGACGGGGATCCAAATAACATGACAAAGCAGT 315  
Qy 346 UAAACUGUAUAGGAAGCUAAGAGGGAGAUAAUUAUUGGAGGCGCCAAAGAAUUCUACU 405  
Db 316 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCATGGGGCCCAAGAAATCTCACT 375  
Qy 406 CAGUUAUUCUGCUGGACUUGCCAGUUAUUGCCGCUCAUAUACACAGGAUUGGGGC 465  
Db 376 CAGTTATTCGTCTGGTGACCTTGGCAGTTGTATGGGCGCTCATATACACAGGATGGGGGC 435  
Qy 466 UGUGACCACUGAAGUGGCAUUGGCUUGGUAUGUGCAACCUUGGAAACAGAUUGCUGACUC 525  
Db 436 TGTGACCACTGAAGTGGCATTTGGCGCTGGTATGTGCAACCTGTGAACAGATTGTGACTC 495  
Qy 526 CCAGCAUCGGUCUAUAGGCAAAUUGGUGAACAACCAACCAUUAUACAGACAUGAGAA 585  
Db 496 CCAGCATCGGTCTCATAGGCAAAATGGTGACAAACCAACCAATCCACTAATCAGACATGAGAA 555  
Qy 586 CAGAAUGUUUAGCCAGCACUACAGCUAAGCUAUGGAGCAAAUGGCUUGGAGUAGCAGUGA 645  
Db 556 CAGAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGGATCGAGTGA 615  
Qy 646 GCAAGCAGCAGAGGCCAGGAGGUUGUAGCAGGCUAGGCAAGGUAAGGCUAGGAGUAG 705  
Db 616 GCAAGCAGCAGAGGCCATGGAGTTGTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG 675  
Qy 706 AACCAUUGGGAUCUAUUCUAGCUCAGCUCAGUGUGUCUGUAAAAUUAUUCUUGAAAAUUU 765  
Db 676 AACCAUUGGGAUCUAUUCUAGCUCAGCUCAGGCTCGAGTCTGAGAAATGATCTCTTGAAAAATTT 735  
Qy 766 GCAGGCCUUAACAGAAACAAUUGGGGUGCAGAGCAACGCUUACAGUAGUAGU 824  
Db 736 GCAGGCCUUAACAGAAACAAUUGGGGUGCAGATGCAACGGTTCAAGTGATCCTCTCGCT 794

RESULT 2

US-11-131-479-45  
; Sequence 45, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; PRIOR FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 45  
; LENGTH: 1305  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Influenza A Virus M1 Fused to Synthetic HbCag  
US-11-131-479-45

Query Match 79.6%; Score 749.6; DB 12; Length 1305;  
Best Local Similarity 77.2%; Pred. No. 2.5e-83;  
Matches 584; Conservative 168; Mismatches 4; Indels 0; Gaps 0;  
Qy 56 AUGAGUCUUAACCGAGGUGCAAGAGUAGUAGUUAUUCUUAUUCUAGGCGGCCUUC 115  
Db 1 ATGAGTCTTCAACCGAGGTCGAAACGTAAGTACTCTCTATCATCCCGTACAGGCCCTC 60

Qy 116 AAAGCCGAGAUCCGACAGAGACUUGAAGAUUGUUCUUGCAGGGAAGAAACCGAUUCUAG 175  
Db 61 AAAGCCGAGATCGACAGAGACTTGAAGATGTCTTTGAGGGAAGAAACACTGATCTTTGAG 120  
Qy 176 GUUCUCAUGGAUUGGCUAAGACAAAGACCAUCCUGACCUUACCUUGACUUAAGGGGAUUUA 235  
Db 121 GTTCTCATGAATGGCTAAAGACAAGACCCTCTGTACCTCTGACTAAGGGATTTTA 180  
Qy 236 GGAUUGUGUUCACGUCUACCGUGCCGAGUGAGCGGAGGACUGCAGCGUAGACGCUUUGUC 295  
Db 181 GGATTTGTGTTACGCTCACCGTGCCAGTGAGCGAGGACTGCGAGCGTAGACGCTTTGTC 240  
Qy 296 CAAAUAUGCCCUUUAUUGGGAACGGGGUCCGGAUUAUUAUUAUUAUUAUUAUUAUUAUUA 355  
Db 241 CAAAATGCCCTTAATGGGAAACGGGGATCCAAATAACATGGAACAAAGCAGTTTAACTGAT 300  
Qy 356 AGGAAGTCAAGAGGGAGUAACAUAUCCAUUGGGGCCAAAGAAUUCUACUCAGUUAUUUC 415  
Db 301 AGGAAGTCAAGAGGGAGATAAATTCATGGGGCCAAAGAAATCTCTCAGTTATCT 360  
Qy 416 GCUUGGCAUCUUGCCAGUUGUUGGCUCAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 475  
Db 361 GCTGGTGCACTTGCCAGTTGTATGGGCTCATATACAACAGGATGGGGCTGTGACCACT 420  
Qy 476 GAAGUGCAUUGGCGUUAUGUAGAACCUUGUAGAACAGUUGUAGUAGUAGUAGUAGUAGUAG 535  
Db 421 GAATGGCAUUGGCGUUAUGUAGAACCUUGUAGAACAGUAGUAGUAGUAGUAGUAGUAGUAG 480  
Qy 536 UCUUAAGGCAUUGGCUAAGCAACCAACCCACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 595  
Db 481 TCTCATAGGCAAAATGGTGACAAACCAATCCACTAATCAGACATGAGAACAGATGGTT 540  
Qy 596 UUAAGCAGCAUACAGCUAAGGCUAUGGAGCAAAUUGGCUAGUAGUAGUAGUAGUAGUAGUAG 655  
Db 541 TTAGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGGATCGAGTGAAGCAGCA 600  
Qy 656 GAGGCCAUGAGGUUUGUAGUAGGCUUAGGCUAAGGCAAAUUGGCUAGGCUAGGCUAGGCUAG 715  
Db 601 GAGGCCATGAGGTTGTAGTCAGGCTAGACAAATGGTGCAAGCGATGGAACCACTTTGGG 660  
Qy 716 ACUACUAGCAGUCCAGUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 775  
Db 661 ACTCATCTAGTCTCAGTGCTGGTCTGAAATAATGATCTCTTGAAATTTTGCAGGCCCTAT 720  
Qy 776 CAGAAACGAUUGGGGUGCAGAUAGCAACGGGUUCAAG 811  
Db 721 CAGAAACGAUUGGGGUGCAGATGCAACGCTTCAAG 756

RESULT 3

US-11-155-478A-131  
; Sequence 131, Application US/11155478A  
; Publication No. US20060014140A1  
; GENERAL INFORMATION:  
; APPLICANT: Boivin, Guy  
; APPLICANT: UNIVERSITE LAVAL  
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING  
; FILE REFERENCE: 6013-148US  
; CURRENT APPLICATION NUMBER: US/11/155,478A  
; CURRENT FILING DATE: 2005-06-20  
; PRIOR APPLICATION NUMBER: CA 2,411,264  
; PRIOR FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: CA 2,418,004  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994  
; PRIOR FILING DATE: 2003-12-19  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 131  
; LENGTH: 987  
; TYPE: DNA

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; ORGANISM: human Influenza A virus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(987)
; OTHER INFORMATION: human Influenza A virus
; OTHER INFORMATION: strain A/Charlottesville/31/95 (H1N1)
; OTHER INFORMATION: accession number af398876
US-11-155-478A-131

Query Match      74.3%; Score 700.2; DB 12; Length 987;
Best Local Similarity 73.7%; Pred. No. 2.7e-77;
Matches 561; Conservative 162; Mismatches 38; Indels 0; Gaps 0;

Qy 56 AUGAGUCUUAACCGAGGUGCAAACGUAUCGUUUCUUAUCCCGUACAGGCCCCUC 115
Db 1 ATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTATCGTCCGTCAGGCCCTC 60

Qy 116 AAAGCCGAGUCCGACAGAGACUUGAAGUUCUUGCAGGGAAGAACACCGAUUUGAG 175
Db 61 AAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCTGGAAGAACACCGCATTTGAG 120

Qy 176 GUUCUCAUGGAUGGCUAAACAGACAGACCAUCCUGUCCACUCUAGUAAGGGGAUUUA 235
Db 121 GCTCTCATGGAGTGCTTAAGACAGACAGACCGATCTGTCTCACCTCTGACTAAGGGGATTTTA 180

Qy 236 GGAUUGUGUUCACGUCACCCGUGCCGAGUGAGCGAGGACUGCAGCGUAGACGCUUUGUC 295
Db 181 GGATTTGTTTCAGCTCACCCTGCCCCAGTGAGCGAGGACTGCGAGCTGAGCGTTTGTGTC 240

Qy 296 CAAAAGUCCCUUAUUGGGAACGGGGAUCCAAUAACAUUGGACAAAGCAGUUUAACUGUUA 355
Db 241 CAAAATGCCCTTAATGGGAATGGGGATCCAAATAACATGGAAGAGCAGAGTAAACCTGTAT 300

Qy 356 AGGAGCUCACAGGGGAGUAACAUUCCNUGGGGCCAAGAAUUCUACUCAGUUAUUCU 415
Db 301 AGAAAGCTTAAGAGGGAGATAACATTCATGGGGCCCAAGAAATAGCACTCAGTTATTCT 360

Qy 416 GCUGGUGCACUUGCGAGUUAUGGGCCUCAUAUAACAACAGAGUGGGGUGUGACCAU 475
Db 361 GCTGGTGCACTTGGCAGTTGTATGGGCTCATATACAACAGATGGGGGCTGTGACCAACC 420

Qy 476 GAAUGGCAUUGGCCUGGUAUGUACAACUUGAACAAGAUUGUGUACUCCAGCAUUGG 535
Db 421 GAATCAGCATTTGGCCTGATATGCGCAACCTGTGAACAGATTGCTGACTCCAGCATAAG 480

Qy 536 UCUCUAUGGCAUUGUGUGACAAACCAACCCACUAUCACACAUGAGAACAGAAUGGU 595
Db 481 TCTCATAGGCAAAATGGTAACAAACCAACCAATCCATTAAAGACATGAGAACAGAAATGTT 540

Qy 596 UUAGCCAGCACACAGCUAAGGCUAUGGCAAAUUGGCUAGUGGAGGAGCAAGCAGCA 655
Db 541 CTGGCCAGCACTACAGCTAAAGCTATGGAGCNAATGGCTGGATCGAGTGAACAAGAGCT 600

Qy 656 GAGGCCAUGGAGGUUGUAGUAGGCUAGGCAAAUUGGCUAGGAGAGAACCAUUGGG 715
Db 601 GAGGCCATGGAGGTTGCTAGTCAGGCCAGGCAAAATGGTGCAGGCAATGAGAGCCATTGGG 660

Qy 716 ACUCAUCCUACUCCAGUGGUCUGGUAAGAAUUAUUAUUGUAAAUAUUGCAGGCCUUA 775
Db 661 ACTCATCTAGCTCTAGCACTGGTCTGAAAAAATGATCTTCTTGAATAATTTGAGGCCCTAT 720

Qy 776 CAGAAACGAUUGGGGUGGACAGAACCAACGGUUAAGUGAAC 816
Db 721 CAGAAACGAATGGGGGTGCAGATGCAACGATTCAAGTGATC 761
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RESULT 4  
US-11-155-478A-130  
; Sequence 130, Application US/11155478A  
; Publication No. US20060014140A1  
; GENERAL INFORMATION:  
; APPLICANT: Boivin, Guy  
; APPLICANT: UNIVERSITE LAVAL

```
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING  
; TITLE OF INVENTION: RESPIRATORY VIRUSES  
; FILE REFERENCE: 6013-148US  
; CURRENT APPLICATION NUMBER: US/11/155.478A  
; CURRENT FILING DATE: 2005-06-20  
; PRIOR APPLICATION NUMBER: CA 2,411,264  
; PRIOR FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: CA 2,418,004  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994  
; PRIOR FILING DATE: 2003-12-19  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 130  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: human Influenza A virus  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)...(1027)  
; OTHER INFORMATION: human Influenza A virus  
; OTHER INFORMATION: strain A/Hong Kong/1180/99 (H3N2)  
; OTHER INFORMATION: accession number af386771  
US-11-155-478A-130
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Query Match      73.2%; Score 689.4; DB 12; Length 1027;
Best Local Similarity 72.1%; Pred. No. 5.5e-76;
Matches 556; Conservative 164; Mismatches 51; Indels 0; Gaps 0;

Qy 46 AGAUCUUAAGAUGAGUCUUAACCGAGGUGGAAACGUAUGUUCUUAUCCGUC 105
Db 16 ATATTGAAAGATGAGCCCTTACCCGAGGTGCGAAACGTATGTTCTCTATCGTTCCATC 75

Qy 106 AGGCCCCUCAAAGCCGAGUCCGACAGAGACUUGAAGUUCUUGCAGGGAAGACAC 165
Db 76 AGGCCCCCTCAAAGCCGAAATCGCGCAGAGACTTGAAGATGCTTTGCTGGGAAGAACAC 135

Qy 166 CGAUUCUUGAGUUCUUAUGGAUGGCUAAGACCAAGACCAUCCUGUCACCUCAUUA 225
Db 136 AGATCTTGAGGCTCTCATGGATGGCTTAAGACAGACCAATCCTGTCACTCTGACTAA 195

Qy 226 GGGGAUUUUAAGGAUUUGUUCUACGUCACCGUGCCCGAGGAGGAGGACUGCAGCGUAG 285
Db 196 GGGGATTTTAGGGTTTGTGTTACGCTCAACGTCGCCAGTGAGCGAGGACTGCGAGCGTAG 255

Qy 286 ACGUUCUUGCCAAAUUGCCCUUAUUGGGAACGGGGAUCCAAUUAACAUAGNCAAGNGU 345
Db 256 ACGCTTTGTCCAAATGSCCTCAATGGGAATGGGGATCCAAATAAACATGGAACAAAGCAGT 315

Qy 346 UAAACUUAUAGGAAGGCUAAGAGGAGUAACAUAUCCAUUGGGGCCAAAGAAUUCUACU 405
Db 316 TAAACTGTATAGAAACCTTAAGAGGGAGATTAACATTCATGGGGCCCAAGANATAGNACT 375

Qy 406 CAGUUAUUCUGGUGGUCACUUGCCUAGUUAUGGGCCUUAUAACAACAGGAGUGGGGGC 465
Db 376 CAGTTATTCTGCTGGTGCACTTCCAGCTTCATGGGCTCATATACAAATAGGATGGGGGC 435

Qy 466 UGUGACCAUAGAGUGSCAUUUGCCUGUUAUGGCAACCCUGGAAACAGAUUGCUGACUC 525
Db 436 TGTAAACCACTGAAAGTGGCATTTTGGCCCTGGTATGTGCAACATGTGAAACAGATTGCTGACTC 495

Qy 526 CCAGGACUGGCUUAUAGGCAAAUUGGUAACAACCAACCCACUAUAACAGACAGUAGAA 585
Db 496 CCAGCAGAGTCTCATAGGCAAAATGTGGCAACACCAACCATCCATTAATAGACATAGAA 555

Qy 586 CAGAAUUGUUUAAGCCAGCAUAACAGCUAAGGCUUAUGGAGCAAAUGGUGGAGUAGUGA 645
Db 556 CAGAAATGGTTTTGGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGCTGATCAAGTGA 615

Qy 646 GCAGCAGCAGAGCCGACUAGGAGUUGCUAGGCUUAGGCAAAUUGGUGGAGGAGUAG 705
Db 616 GCAGGCAGCGGAGGCCATGGAGATTGCTAGTCAGGCCAGGCAAAATGGTGCGAGCAATGAG 675
```













Qy 476 GAAGGCAUUGGCCUGGUAUGUGACUUGGACUUGAAGACAGAUUGUGACUUGCCAGCAUUGG 535  
Db 2072 GAAGTGGCTTTGGCTGGTATGTGCAACATGTGAACAGAGATTGCTGACTCCAGCACAGG 2131  
Qy 536 UCUCAUAGGCAUUGUGGACAAACCAACCAACCAUUAUCACUAGAGAACAGAAUUGGU 595  
Db 2132 TCTCATAGGCAATGGTGGCAACCAACCAATCCATTATTAAGGCGATGAGAACAGAAATGGTT 2191  
Qy 596 UUAAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUUGGUGGUGGUGGUGGUGGAGCAAGCA 655  
Db 2192 TTGGCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGATCAAGTGAAGGAGCGAGCG 2251  
Qy 656 GAGGCCAUGAGGUUGUAGUAGCAGGCUAGGCAAGGCAAAUUGGUGGUGGUGGUGGAG 715  
Db 2252 GAGGCCATGGAAATTTGCTAGTCAGGCCAGGCAAAATGGTGCAGGCAATGAGAGGCCATTGGG 2311  
Qy 716 ACUCAUCCUAGCUCUAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 775  
Db 2312 ACTCATCTAGCTCAGTGTGCTGTCTAAAGATGATCTTCTTGAATTTGACAGACCTAT 2371  
Qy 776 CAGAAACGAUUGGGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 816  
Db 2372 CAGAAACGAUUGGGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 2412

## RESULT 12

US-11-131-479-106  
; Sequence 100, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 100  
; LENGTH: 7798  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VR4769, Ligation of Inverted NP into VR4756  
US-11-131-479-100

Query Match 72.3%; Score 681; DB 12; Length 7798;  
Best Local Similarity 72.0%; Pred. No. 4,1e-75;  
Matches 548; Conservative 163; Mismatches 50; Indels 0; Gaps 0;  
Qy 56 AUGAGUCUUCUACCGAGGUGGAAACGUAAGUUCUUCUUAUCCGUGAGGCGCCCGCUC 115  
Db 1652 ATGAGCTTCTTAACCGAGGTCGAAACGATGTTCTCTATCTGTTCCATCAGGCGCCCTC 1711  
Qy 116 AAAGCCGAUUGGCGACAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 175  
Db 1712 AAAGCCGAUUGGCGACAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1771  
Qy 176 GUUCUUGGAUUGGCUAAAGCAAGACCAUCCUGUACCUUAGUAGUAGUAGUAGUAGUAG 235  
Db 1772 GCTCTCATGGATGGCTAAGACAGACCAATCTCTGCTCCTCTGACTAAGGGATTTG 1831  
Qy 236 GGAUUGUUCACGCUACCGUGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 295  
Db 1832 GGGTTTGTTCACGCTCACCGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1891  
Qy 296 CAAAUGCCCUUUAUGGGAACGGGGAUCCAAUACUAGGACAAAGAGAGUUAACUAGU 355

Db 1892 CAAATGGCTCTCAATGGGAATGGGATCCAAATAACATGACAGAGAGTAAACTATAT 1951  
Qy 356 AGGAAGCUCUACAGGAGGAGUAAUACAUUCCUUGGGCCAAAGAAAUUCUACUAGUUAUUCU 415  
Db 1952 AGAAACTTAAGAGGAGGAGATTACATTCATGGGGCCAAAGAAATAGCACTCAGTTATCT 2011  
Qy 416 GUGGUGCUCUUCGCGAGUUGUUGGCGCUCAUAUACAAAGGAUUGGGGCGUGAGCCACU 475  
Db 2012 GCTGGTGCACTTCCCAAGTTGCATGGGCTCATATAACAAGAAATGGGGGCTGAACCACT 2071  
Qy 476 GAAGUGGCAUUGCGCGUUGUAGUUGCAACCGUGUAAACAGAUUCGUGACUCCAGCAUUGG 535  
Db 2072 GAAGTGGCTTTGGCCCTTGGTATGTGCAACATGTGAACAGATTGCTGACTCCAGCACAGG 2131  
Qy 536 UCUCAUAGGCAUUGGUGAACAACAACCAACCAACCAUUAUACAGUAGAGAAACAGAAUUGGU 595  
Db 2132 TCTCATAGGCAATGGTGGCAACCAACCAATCCATTATTAAGGCGATGAGAACAGAAATGGTT 2191  
Qy 596 UUAAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUUGGUGGUGGUGGUGGUGGUGGAGCA 655  
Db 2192 TTGGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGATCAAGTGAAGGAGCGAGCG 2251  
Qy 656 GAGGCCAUGAGGUUGUAGUAGCAGGCUAGGCAAAUUGGUGGUGGUGGUGGUGGUGGUGG 715  
Db 2252 GAGGCCATGGAAATTTGCTAGTCAGGCCAGGCAAAATGGTGCAGCAATGAGGCCATTGGG 2311  
Qy 716 ACUCAUCCUAGCUCUAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 775  
Db 2312 ACTCATCTAGCTCCAGTGTGCTCTAAAGATGATCTTCTTGAATTTGACAGACCTAT 2371  
Qy 776 CAGAAACGAUUGGGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 816  
Db 2372 CAGAAACGAUUGGGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 2412

## RESULT 13

US-11-131-479-106  
; Sequence 106, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 106  
; LENGTH: 8442  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VR4775, Ligation of RSV RSeg7 into VR4762  
US-11-131-479-106

Query Match 72.3%; Score 681; DB 12; Length 8442;  
Best Local Similarity 72.0%; Pred. No. 4e-75;  
Matches 548; Conservative 163; Mismatches 50; Indels 0; Gaps 0;  
Qy 56 AUGAGUCUUCUACCGAGGUGGAAACGUAAGUUCUUCUUAUCCGUGAGGCGCCCGCUC 115  
Db 6426 ATGAGCTTCTTAACCGAGGTCGAAACGATATGTTCTCTCTATGTTCTCATCAGGCGCCCTC 6485  
Qy 116 AAAGCCGAUUGGCGACAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 175



; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 104  
; LENGTH: 8450  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VR4773, Ligation of RSV RNP into VR4756  
US-11-131-479-104

|                       |      |   |                  |           |              |
|-----------------------|------|---|------------------|-----------|--------------|
| Query Match           |      | 72.3%;  | Score 581;       | DB 12;    | Length 8450; |
| Best Local Similarity |      | 72.0%;  | Pred. No. 4e-75; |           |              |
| Matches 548;          |      | Conservative 163;   | Mismatches 50;   | Indels 0; | Gaps 0;      |
| Qy                    | 56   | AUGAGUCUUCUUAACCGAGGUCGAAACGUACGUUCUCUUAUCCCGUCAGGCGCCUC        | 115              |           |              |
| Db                    | 1652 | ATGAGCCTTCTAACCGAGGTGAAACGATGTTCTCTATCGTTCCATCAGGCCCCCTC        | 1711             |           |              |
| Qy                    | 116  | AAAGCCGAGUUCGACACAGAGACUUGAAGUUCUUGCAGGGAAAGACACCGAUUUGAG       | 175              |           |              |
| Db                    | 1712 | AAAGCCGAAATCGCGCAGAGACTTGAAGATGCTTTGCTGGGAAAAACACAGATCTTGAG     | 1771             |           |              |
| Qy                    | 176  | GUUCUUAUGGAAUGGCUAAGACAGACCAUCCUGUCACCUUGACUAGGGAUUUA           | 235              |           |              |
| Db                    | 1772 | GCTCTCATGGAATGGCTAAAGACAAGACCAATCTGTCTGACTTAAGGGGATTTTG         | 1831             |           |              |
| Qy                    | 236  | GGAUUUGUUCACGUCACCGUCGCCAGUGCGGAGACUGCAGCGUAGACGCUUUGUC         | 295              |           |              |
| Db                    | 1832 | GGGTTTGTTCAGCTCACCCTGCCAGTGCGAGGAGCTGCGAGCTAGACGGCTTTGTC        | 1891             |           |              |
| Qy                    | 296  | CAAAUUGCCCUUUAUGGGAACGGGGAUCCAAAUAAACAUGGACAAAGCAGUUUAAACUGU    | 355              |           |              |
| Db                    | 1892 | CAAAATGCCCTCAATGGGAATGGGATCCAAATAACATGACAGAGCAGTTAAACTATAT      | 1951             |           |              |
| Qy                    | 356  | AGGAAGCUACAGAGGGAUAACAUCUCCAUUGGGGCCAAAGAAUUCACUCAGUUUUCU       | 415              |           |              |
| Db                    | 1952 | AGAAAACTTAAGAGGGAGATTACATTCCATGGGGCCAAAGAAATAGCACTCAGTTATCT     | 2011             |           |              |
| Qy                    | 416  | GCUGGUCACUUGCAGUUGUUGGGCCUUAUACACAGGAGUUGGGGCGUGUACCAU          | 475              |           |              |
| Db                    | 2012 | GCTGGTGACCTTGCAGTTGCTGAGGCTCATATACAACAGATGGGGGCTGTAACTACT       | 2071             |           |              |
| Qy                    | 476  | GAAUGGCAUUGGCGUUGUUGAACACUGUGAACAGAUUGUGACUCCAGCAUCGG           | 535              |           |              |
| Db                    | 2072 | GAGTGGCCTTTGGCCTGGTATGTGCAACATGTGAACAGATTGCTGACTCCAGCAGAG       | 2131             |           |              |
| Qy                    | 536  | UCUUAUGGCAAAUGGUGACAACAACCAACCCACUUAUCAGACAGAGAAUGGUU           | 595              |           |              |
| Db                    | 2132 | TCTCATAGGCAAAATGGTGGCAACCAACCAATCCATTAATAGGCCATGAGAACAGAAATGGTT | 2191             |           |              |
| Qy                    | 596  | UUAGCCAGCACUACAGCUAAGCUAUGGAGCAAAUUGGUGGAGUAGGAGCAAGCAGCA       | 655              |           |              |
| Db                    | 2192 | TTGGCCAGCATTACAGCTAAGGCTATGGAGCNAATGGCTGGATCAAGTAGCAGGCGCG      | 2251             |           |              |
| Qy                    | 656  | GAGGCCAUGGAGGUUGUAGUCAGCUGAGCAAAUUGGUGCAAGCGAUGAGAACCAUUGGG     | 715              |           |              |
| Db                    | 2252 | GAGGCCATGGAAATTTGCTAGTCAGGCCAGGCAAAATGGTGCAGGCAATGAGAGCCATTGGG  | 2311             |           |              |
| Qy                    | 716  | ACUUAUCCUAGCUCGUCGUGGUGAUAAGAAUAGUUAUUCUUGAAAUUUGCAGGCCUUA      | 775              |           |              |
| Db                    | 2312 | ACTCATCTAGCTCAGTGGCTGAAAGATGATCTCTTGAAAAATTTGCAGACCTAT          | 2371             |           |              |
| Qy                    | 776  | CAGAAACGAUUGGGGUGCAGUACGAGCGUUCAGUGAAC                          | 816              |           |              |
| Db                    | 2372 | CAGAAACGAATGGGGGTGCAGATGCACGATTCAGTGACC                         | 2412             |           |              |

Search completed: March 21, 2006, 01:31:34  
Job time : 430.258 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:02:13 ; Search time 190.994 Seconds  
(without alignments)  
8767.110 Million cell updates/sec

Title: US-10-729-830-6

Perfect score: 942

Sequence: 1 gcuuucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaaa 942

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 130357 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
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- 6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
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- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
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| 1          | 488.8 | 51.9        | 4023   | 3     | US-08-809-513A-8   |
| 2          | 487.4 | 51.7        | 1023   | 3     | US-09-506-286B-1   |
| 3          | 487.4 | 51.7        | 1023   | 3     | US-09-762-861B-1   |
| 4          | 487.4 | 51.7        | 1023   | 3     | US-10-065-133A-1   |
| 5          | 487.4 | 51.7        | 1023   | 3     | US-10-434-811A-1   |
| 6          | 486.6 | 51.7        | 6802   | 3     | US-08-809-513A-6   |
| 7          | 484.6 | 51.4        | 1023   | 3     | US-09-506-286B-4   |
| 8          | 484.6 | 51.4        | 1023   | 3     | US-09-762-861B-4   |
| 9          | 484.6 | 51.4        | 1023   | 3     | US-10-065-133A-4   |
| 10         | 484.6 | 51.4        | 1023   | 3     | US-10-434-811A-4   |
| 11         | 477.4 | 50.7        | 816    | 3     | US-09-311-784A-13  |
| 12         | 477.2 | 50.7        | 756    | 3     | US-09-506-286B-3   |
| 13         | 477.2 | 50.7        | 756    | 3     | US-09-762-861B-3   |
| 14         | 477.2 | 50.7        | 756    | 3     | US-10-065-133A-3   |
| 15         | 477.2 | 50.7        | 756    | 3     | US-10-434-811A-3   |
| 16         | 474.4 | 50.4        | 756    | 3     | US-09-506-286B-6   |
| 17         | 474.4 | 50.4        | 756    | 3     | US-09-762-861B-6   |
| 18         | 474.4 | 50.4        | 756    | 3     | US-10-065-133A-6   |
| 19         | 474.4 | 50.4        | 756    | 3     | US-10-434-811A-6   |
| 20         | 473.4 | 50.3        | 1027   | 6     | PCT-US95-12357A-3  |
| 21         | 79.4  | 8.4         | 290    | 3     | US-10-131-827-8418 |
| 22         | 79.4  | 8.4         | 1069   | 3     | US-09-372-422A-7   |
| 23         | 77.6  | 8.2         | 1097   | 3     | US-09-832-129-21   |
| 24         | 76.8  | 8.2         | 569    | 3     | US-09-461-325-44   |

|    |      |     |      |   |                    |                   |
|----|------|-----|------|---|--------------------|-------------------|
| 25 | 76.8 | 8.2 | 569  | 3 | US-10-012-542-44   | Sequence 44, Appl |
| 26 | 76.8 | 8.2 | 569  | 3 | US-10-115-123-44   | Sequence 44, Appl |
| 27 | 76.8 | 8.2 | 3080 | 3 | US-09-099-041A-25  | Sequence 25, Appl |
| 28 | 76.8 | 8.2 | 3080 | 3 | US-09-245-281-25   | Sequence 25, Appl |
| 29 | 76.8 | 8.2 | 3080 | 3 | US-09-207-359B-25  | Sequence 25, Appl |
| 30 | 76.8 | 8.2 | 3080 | 3 | US-09-340-520A-25  | Sequence 25, Appl |
| 31 | 76.8 | 8.2 | 3080 | 3 | US-09-865-364-25   | Sequence 25, Appl |
| 32 | 76.8 | 8.2 | 3080 | 3 | US-09-728-721-25   | Sequence 25, Appl |
| 33 | 76   | 8.1 | 1733 | 3 | US-09-073-569-1    | Sequence 1, Appl  |
| 34 | 75.8 | 8.0 | 990  | 3 | US-09-800-729-79   | Sequence 79, Appl |
| 35 | 75.8 | 8.0 | 1934 | 3 | US-08-776-844-1    | Sequence 1, Appl  |
| 36 | 75.8 | 8.0 | 1934 | 3 | US-09-909-325-1    | Sequence 1, Appl  |
| 37 | 75.8 | 8.0 | 1934 | 3 | US-09-909-326-1    | Sequence 212, App |
| 38 | 75.8 | 8.0 | 1985 | 3 | US-09-907-794A-212 | Sequence 212, App |
| 39 | 75.8 | 8.0 | 1985 | 3 | US-09-905-125A-212 | Sequence 212, App |
| 40 | 75.8 | 8.0 | 1985 | 3 | US-09-902-775A-212 | Sequence 212, App |
| 41 | 75.8 | 8.0 | 1985 | 3 | US-09-906-700-212  | Sequence 212, App |
| 42 | 75.8 | 8.0 | 1985 | 3 | US-09-903-503A-212 | Sequence 212, App |
| 43 | 75.8 | 8.0 | 1985 | 3 | US-09-904-520A-212 | Sequence 212, App |
| 44 | 75.8 | 8.0 | 1985 | 3 | US-09-909-064-212  | Sequence 212, App |
| 45 | 75.8 | 8.0 | 1985 | 3 | US-09-905-381A-212 | Sequence 212, App |

ALIGNMENTS

RESULT 1

US-08-809-513A-8

; Sequence 8, Application US/08809513A

; Patent No. 6524588

; GENERAL INFORMATION:

; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette

; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a

; TITLE OF INVENTION: Method

; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS

; STREET: 660 White Plains Road

; CITY: Tarrytown

; STATE: New York

; COUNTRY: USA

; ZIP: 10591-5144

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage

; COMPUTER: Gateway Pentium II

; OPERATING SYSTEM: Windows 98

; SOFTWARE: Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/809,513A

; FILING DATE: 24-MAR-1997

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP95/03663

; FILING DATE: 18-SEP-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 94115505.3

; FILING DATE: 30-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Kurt G. Briscoe

; REGISTRATION NUMBER: 33,141

; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (914) 332-1700

; TELEFAX: (914) 332-1844

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4023 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO



|    |     |   |     |
|----|-----|---|-----|
| Qy | 526 | CCAGCACGGCAGCACAGGCGAUGUGUAGCACACACCAACCCCCUAGUACGCGCAGAA       | 585 |
| Db | 495 | CCAGCATCGATCTCACAGGCGAGATGGTGACAACAAACCAACCCATTAATTCAGACATGAAAA | 554 |
| Qy | 586 | CAGGAUGGUGUGUGGCCAGCAGCACACCGCCAGGCCAUGAGCAGAUUGCGCGGAGCAGCGA   | 645 |
| Db | 555 | CAGAAATGGTATTAGCCAGTACCAACGGCTTAAGCCCATGGAGCAGATGGCAGGGTCAGTGCA | 614 |
| Qy | 646 | CGAGGCCGCGAGGCCAUGGAGGUGGCCAGCCAGCCAGGCGAUGUGUGUGCGCCAUAG       | 705 |
| Db | 615 | CGAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTTCAGGCAATGAG    | 674 |
| Qy | 706 | GACCAUCGGCACCCACCCAGCAGCAGCGCGCGCUGAAGAACGACCUUGUCGAGAACCU      | 765 |
| Db | 675 | AACCAATTGGGACCCACCCTAGCTCAGTGCAGGTTTGAAGATGATCTCCTTGAANAATT     | 734 |
| Qy | 766 | CGAGGCCUACCAAGAGCGCAUGGCGUGUGCAGAUAGCAGCGCUUCAAUGAAC            | 816 |
| Db | 735 | CGAGGCTTACCAAGAAACGGATGGGAGTGCAAATCGAGCGATTCAAGTGATC            | 785 |

```

US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18593
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

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| Query Match               | Score | DB 3              | Length   |
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| Best Local Similarity     | 51.7% | 487.4             | 1023     |
| Matches 501: Conservative | 65.0% | Pred. No. 6.8e-74 |          |
| Matches 501: Conservative | 93    | Mismatches 177    | Indels 0 |
|                           |       |                   | Gaps 0   |

|    |     |  |     |
|----|-----|--|-----|
| Qy | 46  | AGAUCAAAGUAGAGCCUGUGACCGAGGUGGAGACCUACGUGUGAGCAUACUCCCG      | 105 |
| Db | 15  | ATATTTAAAGATGAGTCTTCTGACCGAGGTGGAACGCTACTCTCTCTCTGTAACCATC   | 74  |
| Qy | 106 | CGGCCCCUGAAGGCCGAGAUCCGCCAGAGGCGUGAGGACGAGUUGCGCGGCAAGAACAC  | 165 |
| Db | 75  | AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGCTCTTGCAGGGAGAACAC  | 134 |
| Qy | 166 | CGACCCGAGGUGUGAUGGAGUGGCGUGAAGACGAGGCCAUCCUGAGCCCCCUGACCAA   | 225 |
| Db | 135 | CGATCTTGAGGCATCTGNAATGCGTAAGACAAGCAACCAATCCTGTCACTCTGACTAA   | 194 |
| Qy | 226 | GGGCAUCCUGGGCUUUGUUGUACCUCCUGA CCGUGCCAGCGAGCGCGGCGUGACGGCCG | 285 |
| Db | 195 | AGGATTTTAGGATTTGATTTACGGCTCACCGTCCAGTGAGGAGGAGCTCAGCGTAG     | 254 |

| Query Match           | 51.7% | Score 487.4  | DB 3           | Length 1023 |
|-----------------------|-------|--|----------------|-------------|
| Best Local Similarity | 65.0% | Pred. No. 6.8e-74  |                |             |
| Matches               | 501   | Conservative 93  | Mismatches 177 | Indels 0    |
| Qy                    | 46    | AGAUCUAAAGUAGCCUCGUCAGCCGAGGUAGAGACCUAGUCGUCGAGCAUCAUCCCCAG      | 105            |             |
| Db                    | 15    | ATATTTAAAGATGAGTCTTCTGACCGAGGTGCAAAACGTACGTTCTCTATATCGTACCATC    | 74             |             |
| Qy                    | 106   | CGGCCCCUCUAGAAGCCGAGAUUCGCCAGAGGCGGAGACGUGUUCGCCGCAAGAACAC       | 165            |             |
| Db                    | 75    | AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAGATGCTTTGCGAGGGAAGAACAC      | 134            |             |
| Qy                    | 166   | CGACCGUAGAGUGUCUAGUGGAGUGGCGUGAAGACGAGGCCCAUCCUGAGCCCCUGACCAA    | 225            |             |
| Db                    | 135   | CGATCTTTGAGGCACTCATATGGAATGGCTAAAGACAAGACCAATCCTGTCAACCTCTGACTAA | 194            |             |
| Qy                    | 226   | GGGCAUCCUGGGCUUUCUGUUGUACCCUUGAACCGUGCCGACGAGCGCGCGCUCUGAGCGCG   | 285            |             |
| Db                    | 195   | AGGGATTTTAGGATTCGTATTTCAGCGCTCACCGTCCCACTGAGCGAGGACTGCGACGGTAG   | 254            |             |
| Qy                    | 286   | CCGCUUCUGCAGACGACCCUAGACGGCAACGGCGACCCCAACAACGAUGGACAGAGCCGU     | 345            |             |
| Db                    | 255   | ACGCTTTGTTCCAAATGCCCTTAGTGGAACGAGATCCAAACAACATGGACAGACGAGT       | 314            |             |
| Qy                    | 346   | GAAGCUCUACAGGAAGCUGAAGAGGGAGAUACACUCCAGCGGCCCAAGGAGAUACAGCCT     | 405            |             |
| Db                    | 315   | AAAACTGTACAGGAAGCTTAAAGAGAATAACAATTCATGGGGCAAAAGAGGTGGCACT       | 374            |             |
| Qy                    | 406   | GAGCUACAGCGCCGCGCCUCUGGCAGCGUAGUGGGCCUGAUCAACAGGAUUGGGCGC        | 465            |             |
| Db                    | 375   | CAGCTATTCCACTGSGTCACTAGCCAGCTGCTGGGACTCATATACAACAGAAATGGGAAC     | 434            |             |
| Qy                    | 466   | CGUGACCAACCGAGUGGCUUUCUGGCCUUGGUGUGGCCCAACCUUGCGAGCAGAUUCGCCAG   | 525            |             |
| Db                    | 435   | TGTGACAAACCGAAGTGGCATTTGGCTTGGTATGCGGCACATGTGAAACAGATCGTGAATC    | 494            |             |















Db 241 CAAATGCCCTTAGTGGAAACGGAGATCCAAACACATGGACAGAGCAGTAAACACTGTAC 300  
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Db 301 AGGAAGCTTAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360  
Qy 416 GCCGGCCCGUGGCGAGCUGCAUGGCGCCUGAUCAACAGGAGUUGGGCGGUGUACCAACC 475  
Db 361 ACTGGTGCACTAGCCAGCTGATGGGACTCATATACAAACAGAAATGGGAACCTGTGACAACC 420  
Qy 476 GAGGUGGCCUUGCGGUGUGUGCGCCACUGCGAGCAGAUUGCGGCAGCCAGCAGCGC 535  
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Qy 536 AGCCACAGGAGAGUGGAGCACCACCAACACCCUGAUCAGGACGAGAACAGAGUGGUG 595  
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Qy 596 CUGGCCAGCACACCGCAAGGCCAUGAGAGAGAUUGGCGGCAGCAGCAGCGCCGCC 655  
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Db 601 GAGGCCATGAGGTGTCTAGTAAGCGTAGGCAGATGGTTCAGGCAATGAGAACCATTTGGG 660  
Qy 716 ACCCACCCAGCAGCAGCGCCGCCUGAAGAACGACCUUGUGGAGAACCUUGAGCCUAC 775  
Db 661 ACCCACCTAGCTCCAGTGCCTTTGAAAGATGATCTCCTTGAATAATTTGCAGGCCCTAC 720  
Qy 776 CAGAAGCGCAUGGCGUGAGAGUAGCAGCGCUUCAAAG 811  
Db 721 CAGAAGCGGATGGGAGTGCAATGCAGCGATTCAAG 756

## RESULT 15

US-10-434-811A-3  
; Sequence 3, Application US/10434811A  
; Patent No. 6824784  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EO-1-C1-PUS-1  
; CURRENT APPLICATION NUMBER: US/10/434,811A  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-434-811A-3

Query Match 50.7%; Score 477.2; DB 3; Length 756;  
Best Local Similarity 65.1%; Pred. No. 3.5e-72;  
Matches 492; Conservative 90; Mismatches 174; Indels 0; Gaps 0;  
Qy 56 AUGAGCCUGUGCAGCGAGGUGAGACCUACCGUGUGAGCAUCCGCCAGCGGCCCGCCUG 115  
Db 1 ATGAGTCTTTCAGCCGAGGTGGAACGCTACGTTCTCTATCGTACCAATCAGGCCCCCTC 60  
Qy 116 AAGCCGAGAUUGCCCGAGGCGUGGAGGAGCUGUUGCGCGGCAAGAAACACCGACCUAGG 175  
Db 61 AAACCCGAGATCGCGCAGAGACTTGAAGATGCTTTGCGAGGGAAGAACCCGATCTTGAG 120

Qy 176 GUCUGAUGGAGUGGUGAGAGACAGGCCCAUCCUGAGCCGCCUUGACCAAGGGAUCCUG 235  
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Qy 536 AGCCACAGGAGAGUGGAGCACCACCAACCCUGAUCAGGACGAGAACAGAGUGGUG 595  
Db 481 TCTCACAGGCAGATGGTGACAAACCAACCCATTATCAGACATGAACAGAAATGGTA 540  
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Db 541 TTAGCCAGTACACCGGTAAAGCCATGGAGCAGATGGCAGGTTCGAGTGAGCAGGCAGCA 600  
Qy 656 GAGGCCAUGGAGUGGCGCAGCCAGGCGCAGCAGAUUGGUGAGCGCAUUGAGGAACUUGCGC 715  
Db 601 GAGGCCATGAGGTGTCTAGTAAGCGTAGGCAGATGGTTCAGGCAATGAGAACCATTTGGG 660  
Qy 716 ACCCACCCAGCAGCAGCGCCGCCUGAAGAACGACCUUGUGGAGAACCUUGAGCCUAC 775  
Db 661 ACCCACCTAGCTCCAGTGCCTTTGAAAGATGATCTCCTTGAATAATTTGCAGGCCCTAC 720  
Qy 776 CAGAAGCGCAUGGCGUGAGAGUAGCAGCGCUUCAAAG 811  
Db 721 CAGAAGCGGATGGGAGTGCAATGCAGCGATTCAAG 756

Search completed: March 20, 2006, 23:50:27

Job time : 192.994 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:29:50 ; Search time 925.936 Seconds  
(without alignment)  
8412.838 Million cell updates/sec

Title: US-10-729-830-6  
Perfect score: 942  
Sequence: 1 gcuugucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaaaa 942

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
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8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description      |
|------------|-------|---------------|--------|-------|------------------|
| 1          | 942   | 100.0         | 942    | 8     | US-10-729-830-6  |
| 2          | 884   | 93.8          | 1011   | 8     | US-10-729-830-7  |
| 3          | 775   | 82.3          | 775    | 8     | US-10-729-830-3  |
| 4          | 762   | 80.9          | 844    | 8     | US-10-729-830-4  |
| 5          | 666.8 | 70.8          | 942    | 8     | US-10-729-830-5  |
| 6          | 498.8 | 53.0          | 774    | 8     | US-10-729-830-1  |
| 7          | 497   | 52.8          | 986    | 8     | US-10-866-484-9  |
| 8          | 489.4 | 52.0          | 1027   | 6     | US-10-177-390-31 |
| 9          | 487.8 | 51.8          | 1027   | 8     | US-10-855-875-5  |
| 10         | 487.4 | 51.7          | 1023   | 6     | US-10-065-133A-1 |
| 11         | 487.4 | 51.7          | 1023   | 7     | US-10-434-811A-1 |
| 12         | 487.4 | 51.7          | 1023   | 7     | US-10-734-373-1  |
| 13         | 487.4 | 51.7          | 1023   | 8     | US-10-872-014-1  |
| 14         | 484.6 | 51.4          | 1023   | 6     | US-10-065-133A-4 |
| 15         | 484.6 | 51.4          | 1023   | 7     | US-10-434-811A-4 |
| 16         | 484.6 | 51.4          | 1023   | 7     | US-10-734-373-4  |
| 17         | 484.6 | 51.4          | 1023   | 8     | US-10-872-014-4  |
| 18         | 477.4 | 50.7          | 816    | 6     | US-10-371-025-13 |
| 19         | 477.4 | 50.7          | 816    | 6     | US-10-371-069-13 |
| 20         | 477.4 | 50.7          | 816    | 6     | US-10-371-645-13 |
| 21         | 477.4 | 50.7          | 816    | 6     | US-10-371-260-13 |
| 22         | 477.2 | 50.7          | 756    | 6     | US-10-065-133A-3 |
| 23         | 477.2 | 50.7          | 756    | 7     | US-10-434-811A-3 |

|      |       |      |      |   |                      |                    |
|------|-------|------|------|---|----------------------|--------------------|
| 24   | 477.2 | 50.7 | 756  | 7 | US-10-734-373-3      | Sequence 3, Appli  |
| 25   | 477.2 | 50.7 | 756  | 8 | US-10-872-014-3      | Sequence 3, Appli  |
| 26   | 474.6 | 50.4 | 1002 | 3 | US-09-747-335-3      | Sequence 3, Appli  |
| 27   | 474.6 | 50.4 | 1002 | 7 | US-10-435-723A-3     | Sequence 3, Appli  |
| 28   | 474.4 | 50.4 | 756  | 6 | US-10-065-133A-6     | Sequence 6, Appli  |
| 29   | 474.4 | 50.4 | 756  | 7 | US-10-434-811A-6     | Sequence 6, Appli  |
| 30   | 474.4 | 50.4 | 756  | 7 | US-10-734-373-6      | Sequence 6, Appli  |
| 31   | 474.4 | 50.4 | 756  | 8 | US-10-872-014-6      | Sequence 6, Appli  |
| 32   | 473.4 | 50.3 | 1027 | 7 | US-10-381-530-7      | Sequence 3, Appli  |
| 33   | 472.6 | 50.2 | 759  | 8 | US-10-617-569-3      | Sequence 3, Appli  |
| 34   | 88.8  | 9.4  | 1476 | 3 | US-09-374-046A-83    | Sequence 83, Appli |
| 35   | 88.8  | 9.4  | 1476 | 7 | US-10-616-263-83     | Sequence 83, Appli |
| C 36 | 84.2  | 8.9  | 573  | 7 | US-10-424-599-135848 | Sequence 135848,   |
| C 37 | 83.4  | 8.9  | 362  | 8 | US-10-425-115-68338  | Sequence 68338, A  |
| C 38 | 83    | 8.8  | 598  | 7 | US-10-021-323-11423  | Sequence 11423, A  |
| C 39 | 82.8  | 8.8  | 510  | 7 | US-10-437-963-1928   | Sequence 1928, Ap  |
| C 40 | 82.6  | 8.8  | 374  | 7 | US-10-437-963-32121  | Sequence 32121, A  |
| C 41 | 82    | 8.7  | 405  | 8 | US-10-425-115-76344  | Sequence 76344, A  |
| C 42 | 82    | 8.7  | 554  | 7 | US-10-021-323-4489   | Sequence 4489, Ap  |
| C 43 | 82    | 8.7  | 1714 | 8 | US-10-425-115-170894 | Sequence 170894,   |
| C 44 | 81.6  | 8.7  | 559  | 7 | US-10-021-323-14094  | Sequence 14094, A  |
| C 45 | 81.6  | 8.7  | 585  | 8 | US-10-425-115-169902 | Sequence 169902,   |

ALIGNMENTS

RESULT 1  
US-10-729-830-6  
; Sequence 6, Application US/10729830  
; Publication No. US20050032730A1  
; GENERAL INFORMATION:  
; APPLICANT: Von der Muelbe, Florian  
; APPLICANT: Hoerr, Ingmar  
; APPLICANT: Pascolo, Steve  
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA  
; FILE REFERENCE: 2793-1-001PCT/CIP  
; CURRENT APPLICATION NUMBER: US/10/729,830  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: PCT/EP02/06180  
; PRIOR FILING DATE: 2002-06-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 942  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Influenza  
; OTHER INFORMATION: matrix: mRNA with increased G/C-content and  
; OTHER INFORMATION: stabilisation sequences  
; FEATURE:  
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-  
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,  
; OTHER INFORMATION: respectively.  
; FEATURE:  
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop  
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)  
US-10-729-830-6

Query Match 100.0%; Score 942; DB 8; Length 942;

Best Local Similarity 100.0%; Pred. No. 4.5e-182; Indels 0; Gaps 0;  
Matches 942; Conservative 0; Mismatches 0;

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|----|----|---|
| Qy | 1  | GCUGUUCUUUUUGCAGAGCUCAGAAUAAACGCUCUAACUUGGCAGACUAAAGAUAGAG 60 |
| Db | 1  | GCUGUUCUUUUUGCAGAGCUCAGAAUAAACGCUCUAACUUGGCAGACUAAAGAUAGAG 60 |
| Qy | 61 | CCUGUGACCGAGGUGGAGACCUAGCUGUGAGCAUCAUCCCCCGCCCCCUUGAAGGC 120  |
| Db | 61 | CCUGUGACCGAGGUGGAGACCUAGCUGUGAGCAUCAUCCCCCGCCCCCUUGAAGGC 120  |



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Qy 121 CGAGAUCCGCCAGAGGCTUGGAGGACGUGUUCGCCGCGCAAGAACACCCAGCACCUGGAGGUGCU 180
Db 121 CGAGAUCCGCCAGAGGCTUGGAGGACGUGUUCGCCGCGCAAGAACACCCAGCACCUGGAGGUGCU 180
Qy 181 GAUGGAGUGGCTUGAAGACCAAGCCCAUCCUGAGGCCCTUGACCAAGGCGCAUCCUGGCGCU 240
Db 181 GAUGGAGUGGCTUGAAGACCAAGCCCAUCCUGAGGCCCTUGACCAAGGCGCAUCCUGGCGCU 240
Qy 241 CGUUGUACCCUGACCGUGGCCAGCGAGCGCGGCTUGAGCGCGCGCTUGUUGUGAGAA 300
Db 241 CGUUGUACCCUGACCGUGGCCAGCGAGCGCGGCTUGAGCGCGCGCTUGUUGUGAGAA 300
Qy 301 CGCCUGAAACGCGCAACGGCGACCCCAACAAUGGACAAAGGCCGUGAAGGUGUACAGAA 360
Db 301 CGCCUGAAACGCGCAACGGCGACCCCAACAAUGGACAAAGGCCGUGAAGGUGUACAGAA 360
Qy 361 GCUCAAGAGGAGAUCACTUCCACCGCGCAAGGAGAUCAAGCGCTUGAGCUACAGCGCGG 420
Db 361 GCUCAAGAGGAGAUCACTUCCACCGCGCAAGGAGAUCAAGCGCTUGAGCUACAGCGCGG 420
Qy 421 CGCCCTUGGCCAGTUGCAUGGGCTUGAUCAACAGGAGUGGCGCGCTUGACCAACCGAGGU 480
Db 421 CGCCCTUGGCCAGTUGCAUGGGCTUGAUCAACAGGAGUGGCGCGCTUGACCAACCGAGGU 480
Qy 481 GGCCTUGCGCTUGGUGCGCCACCTUGGAGCAGAUCCGCGACAGUCCGCGACGACCGAGCCA 540
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Qy 541 CAGGACAGUGGAGACCAACCAACCCCTUGCAUAGGCGCAGACGACGAGGAGGUGGCTUGGC 600
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Qy 601 CAGCACCAACCGCCAGGCGCAUGGAGCAGAUUGGCGCGCAGCAGCGCGCGAGGC 660
Db 601 CAGCACCAACCGCCAGGCGCAUGGAGCAGAUUGGCGCGCAGCAGCGCGCGAGGC 660
Qy 661 CAUGGAGUGGCGCAGCGCCGUGAAGACGACCTUGTUGGAGAACCTUGAGGCGCTUACCGAA 720
Db 661 CAUGGAGUGGCGCAGCGCCGUGAAGACGACCTUGTUGGAGAACCTUGAGGCGCTUACCGAA 720
Qy 721 CCCAGCAGCAGCGCGCGCTUGAAGACGACCTUGTUGGAGAACCTUGAGGCGCTUACCGAA 780
Db 721 CCCAGCAGCAGCGCGCGCTUGAAGACGACCTUGTUGGAGAACCTUGAGGCGCTUACCGAA 780
Qy 781 GCGAUGGCGGUGCAGUAGCAGCGCTUUCAGUGAACTUAGUGACUAGCAGCAGCGCGCGC 840
Db 781 GCGAUGGCGGUGCAGUAGCAGCGCTUUCAGUGAACTUAGUGACUAGCAGCAGCGCGCGC 840
Qy 841 CUCCCAACGGGCTUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCC 900
Db 841 CUCCCAACGGGCTUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCC 900
Qy 901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
Db 901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
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RESULT 2
US-10-729-830-7
; Sequence 7, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1011
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA coding for secreted form with
; OTHER INFORMATION: increased G/C-content and stabilisation sequences
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 881 to 883)
US-10-729-830-7

Query Match 93.8%; Score 884; DB 8; Length 1011;
Best Local Similarity 100.0%; Pred. No. 2.9e-170;
Matches 884; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 AGCTUCUGACGAGGUGGAGACCTUACGUGCUGAGCAUACCCAGCGGCCCCCUAAG 118
Db 128 AGCTUCUGACGAGGUGGAGACCTUACGUGCUGAGCAUACCCAGCGGCCCCCUAAG 187
Qy 119 GCCGAGAUCCGCCAGAGGCTUGGAGGACGUGUUCGCCGCGCAAGAACACCGACCUAGGUG 178
Db 188 GCCGAGAUCCGCCAGAGGCTUGGAGGACGUGUUCGCCGCGCAAGAACACCGACCUAGGUG 247
Qy 179 CUGAUGGAGUGGCTUGAAGACGAGCCCAUCCUGAGGCCCTUGACCAAGGCGAUCCUGGGC 238
Db 248 CUGAUGGAGUGGCTUGAAGACGAGCCCAUCCUGAGGCCCTUGACCAAGGCGAUCCUGGGC 307
Qy 239 UUCGUGUACCTUCGACCGGCGCAGGCGCGGCTUGCAGCGCGCGCTUGCAGCGCGCTUCUGGCG 298
Db 308 UUCGUGUACCTUCGACCGGCGCAGGCGCGGCTUGCAGCGCGCGCTUGCAGCGCGCTUCUGGCG 367
Qy 299 AAGCCCTCUGAAACGCGCAACGCGCGACCCCAACAAUAGGACAAAGGCGGUGAAGCUGUACAGG 358
Db 368 AAGCCCTCUGAAACGCGCAACGCGCGACCCCAACAAUAGGACAAAGGCGGUGAAGCUGUACAGG 427
Qy 359 AAGCTUGAAGAGGAGGAUACCTUUCGCGCGCCAGGAGAUACAGCTUGAGCUACAGCGCC 418
Db 428 AAGCTUGAAGAGGAGGAUACCTUUCGCGCGCCAGGAGAUACAGCTUGAGCUACAGCGCC 487
Qy 419 GGGCGCTCUGGCGCAGCTUGCAUGGGCTUGAUCAACAAAGGAGUGGCGCGCTUGACCAACGAG 478
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Qy 479 GUGGCTUUCGGCTCUGGUGUGCGCCACCTUGCGAGCAGAUCCGCGCAGCAGCAGCAGCGCAGC 538
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Qy 539 CACAGGCGAUGGUGACCAACCAACCCCTUGAUAAGGCAAGGAGAAAGAGGUGGUGUG 598
Db 608 CACAGGCGAUGGUGACCAACCAACCCCTUGAUAAGGCAAGGAGAAAGAGGUGGUGUG 667
Qy 599 GCCAGCACCAACCGCCAGGCGCAUGGAGCAGUAGCGCGCAGCAGCAGGAGCGCGCGCAG 658
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Qy 659 GCCAUGGAGGUGGCGCAGCGCGCAGGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 718
Db 728 GCCAUGGAGGUGGCGCAGCGCGCAGGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 787
Qy 719 CACCCAGCAGCAGCGCGCTUGAAGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 778
Db 788 CACCCAGCAGCAGCGCGCTUGAAGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 847
Qy 779 AAGCGCAUGGCGGCTUGAGGAGGCGCTUACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 838
Db 848 AAGCGCAUGGCGGCTUGAGGAGGCGCTUACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 907
Qy 839 GCTUCCCAACGCGGCGCTUCCCGCTUCCCGCTUCCCGCTUCCCGCTUCCCGCTUCCCGCTUCC 898
Db 908 GCTUCCCAACGCGGCGCTUCCCGCTUCCCGCTUCCCGCTUCCCGCTUCCCGCTUCCCGCTUCC 967
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QY 899 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
Db 968 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011

RESULT 3
US-10-729-830-3
; Sequence 3, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; PRIOR FILING DATE: 2003-12-05
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 775
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: gene with increased G/C-content
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
US-10-729-830-3
Query Match 82.3%; Score 775; DB 8; Length 775;
Best Local Similarity 87.7%; Pred. No. 4.1e-148;
Matches 680; Conservative 95; Mismatches 0; Indels 0; Gaps 0;

QY 46 AGAUCUUAAGUAGCCUUGUCGAGCGAGGUGGAGACUACUGUCGAGCAUCCCCAG 105
Db 1 AGATCTAAAGATGAGCCCTGCTGACCGAGGTGGAGACCTACGTGTGACATCCCCAG 60
QY 106 CGGCCCCUAGAGGCCGAGAUCCGCCAGAGGUGGAGACUGUUCGCCGCAAGAAC 165
Db 61 CGGCCCTTGAAGCCGAGATGCGCCAGAGGCTGGAGACGTGTCGCCGCAAGAAC 120
QY 166 CGACUUGAGGUGUCUAGUGGAGUGGUGUGAAGACAGGCCCAUCCUGAGCCCC 225
Db 121 CGACCTGAGGTGCTGATGAGTGGCTGAAGACAGGCCCATCTGTAGCCCCCTG 180
QY 226 GGGCAUCCUGGCUUGUUCUACCCUGACCGUGGCCAGCGCGGCGGCGGCGCG 285
Db 181 GGGCATCTGGGCTTTCGTGTTTACCCCTGACCGTCCCGAGCGCGGCGGCGGCG 240
QY 286 CGGUUUCUGAGAACGCCUUGAACGCAAGCGGACCCCAACCAUUGAACAAGCCG 345
Db 241 CGCTTCTGTGNAAGCCCTTGAACGGCAAGCGGACCCCAACCAATGGACAGCC 300
QY 346 GAAUGCUUACAGGAAGCUGAAGAGGAGAUCAUCCUCCAGCGCGCAAGAGAUAG 405
Db 301 GAAAGTGTACAGGAAGCTGAAGAGGAGATCACCTTCCAGCGCGCAAGGAGATC 360
QY 406 GAGCUACAGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 465
Db 361 GAGCTACAGCGCGCGCGCGCTGGCCAGCTGTGAGGCGCTGTATCTACAAAGG 420
QY 466 CGUGACCAACCGAGGUGGCUUUGCGGCTUGGUGGCGGCGGCGGCGGCGGCG 525
Db 421 COTGACCAACCGAGGTGGGCTTTCGGCTGTGTGCGCCACCTGCGAGGAGATCG 480
QY 526 CCAGCACCGACGCCACAGGAGUGGUGACCAACCAACCCUUGAUAGCGACGAG 585
Db 585 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011

US-10-729-830-4
US-10-729-830-4
; Sequence 4, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; PRIOR FILING DATE: 2003-12-05
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 844
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: gene for secreted form (with N-terminal
; OTHER INFORMATION: signal sequence) with increased G/C-content
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 836 to 838)
US-10-729-830-4
Query Match 80.9%; Score 762; DB 8; Length 844;
Best Local Similarity 87.9%; Pred. No. 1.8e-145;
Matches 670; Conservative 92; Mismatches 0; Indels 0; Gaps 0;

QY 59 AGCUGUGACCGAGGUGGAGACUACUGUCUGAGCAUACUCCAGCGGCCCGCUGA 118
Db 83 AGCCTGTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGA 142
QY 119 GCCGAGUCCGCCAGAGCGUGGAGGACUGUUCGCCGCAAGACACCGACCUAGG 178
Db 143 GCCGAGATCCGCCAGAGGCTGGAGGACGTGTTCGCCGCAAGAACACCGACCT 202
QY 179 CUGAUGAGUGGCGUGAAGAGACAGGCCCAUCCUGAGCGGCCUAGCAAGGGCA 238
Db 203 CTGATGAGTGGCTGAAGACACGAGCCCATCTGTAGCGGCCCTGTACCAAGGG 262
QY 239 UUCGUGUUAUCCUAGACCGUGCCAGCGAGCGGCGGCGGCGGCGGCGGCGG 298
Db 263 TTGCTGTTACCCCTGACCGTGCAGCGCGGCGGCGGCGGCGGCGGCGGCGG 322
QY 299 AACGCCUUAACCGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 358
Db 323 AACGCCCTGAACCGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 382
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Qy 359 AAGCTGAAGAGGAGAUACCUUCCACGGCGCCCAAGGAGUAUCGCTUGAGCUACAGCGCC 418
Dy 383 AAGCTGAAGAGGAGATCACCTTCCACGGCGCCCAAGGAGATCACGCTGAGCTACAGCGCC 442
Qy 419 GGGCCCTTGGCCAGCTGATGGGCTGTATCTAACAAGGATGGGCGCGGTGACCAACCGAG 478
Dy 443 GGGCCCTTGGCCAGCTGATGGGCTGTATCTAACAAGGATGGGCGCGGTGACCAACCGAG 502
Qy 479 GUGGCCUUGCGCCUGUGUGCGCCACCTUGGAGCAGAUUGCCGACAGCCAGCAGCCGAGC 538
Dy 503 GTGGCCCTTGGCGCTGGTGTGGCCACCTGCGAGCAGATCGCCGACAGCAGCAGCCGAGC 562
Qy 539 CACAGGAGAGUGGAGACCAACACCAACCCCTGAGAGGACGACGAGACAGAGAGUGGUG 598
Dy 563 CACAGGAGAGTGGTGACCAACCAACCCCTGATCAGGCAAGGAGACAGAGTGGTGTG 622
Qy 599 GCCAGCACCCCGCCAGAGGCAUGGAGCAGAGUGGCGCGCAGCAGCAGCGCGCGCGAG 658
Dy 623 GCCAGCACCCCGCCAGAGGCAUGGAGCAGATGGCGCGCAGCAGCAGCGCGCGCGAG 682
Qy 659 GCCAUGGAGUGGCGCAGCAGCGCCAGGCGCAGAGUGGCGCAUGAGGACCAUCGCGCAC 718
Dy 683 GCCATGAGGTGGCGCAGCAGCGCCAGGCGCAGATGGTGCAGGCGCATGAGGACCATCG 742
Qy 719 CACCCAGCAGCAGCGCGCGCGCGCGCAGAGAACGACCTUGGAGAGACCTUGCAGGCG 778
Dy 743 CACCCAGCAGCAGCGCGCGCGCGCGCGCAGAGAACGACCTGTGGAGAACCTGCGAGCG 802
Qy 779 AAGCGCAUGGCGGUGGAGAGCAGCGCUUCAAAGUGNACUAGU 820
Dy 803 AAGCGCATGGGCGTGCAGATCAGCGCTTCAAGTGAACACTAGT 844
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RESULT 5
; Sequence 5, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE OF INVENTION: Optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729.830
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-5
```

```
Query Match 70.8%; Score 666.8; DB 8; Length 942;
Best Local Similarity 81.7%; Pred. No. 4.4e-126;
Matches 770; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

Qy 1 GCUUGUUCUUUUGCAGAGCUCAGAAUAAACGCUCAUUGGCGAGAUCAUAAAGUAG 60
Dy 1 GCUUGUUCUUUUGCAGAGCUCAGAAUAAACGCUCAUUGGCGAGAUCAUAAAGUAG 60
```

```
Qy 61 CCUGTUGACGAGGUGGAGACCUUACGUGUGAGCAUCCUCCAGCGGCGCCCGCCUAGAGGC 120
Dy 61 UCUUUUAAACGAGGUGCGAAACGUAUUCUCUUAUCCCGUGAGGCGCCCGCCUAAAGC 120
Qy 121 CGAGAUUGCGCCAGAGGUGGAGGACGUGUUGCGCGGCAAGAACACCGACGUGAGGUGCU 180
Dy 121 CGAGAUUGCGCACAGAGACUUGAGAGUGUUGGAGCGGAGAGAACACCGAUUUGAGGUUC 180
Qy 181 GAUGGAGUGGCGUAAAGACACAGGCGCCAUCCUGAGCGCCUUGAACCAAGGCAUCCUGGGCU 240
Dy 181 CAUGGAUUGCGUAAAGACAAAGACCAUCCUGUACCCUCUGACUAAGGGGAUUTUAGAU 240
Qy 241 CGUUGUACCCUGACCGUGCGCCAGCGCGCGUGCAGCGCGCGCGCGCGCGCGUGCAGAA 300
Dy 241 UGUUGUACCGUCACCGUGCGCCAGUGAGCGAGGACUGCAGCGUAGACGCGUUUGUCCAAA 300
Qy 301 CGCCUUGAACCGGCAACGGCGACCCCAACAACAUAGCAAGGCGCGUGAAGCUGUACAGGAA 360
Dy 301 UGCCUUUAUGGGAACGGGGAUCCAAUAUAUGGACAAAGGAGAUUAACUGUAAGGAA 360
Qy 361 GCUAAAGAGGAGAUCAUCCUCCACCGCGCCAAAGGAGAUCCAGCCUGAGCUACAGCGCG 420
Dy 361 GCUCAAAGAGGAGAUCAUCCUCCACCGCGCCAAAGGAGAUCCAGCCUGAGCUACAGCGCG 420
Qy 421 CGCCUUGCGCAGCUGCAUGGCGCGUGAUCAUACAGAGAGUGGCGCGCGCGCGCGCGAGU 480
Dy 421 UGCACUUGCGAGUUGAUUGGCGCGCUCAUAAUCAAAGAGUGGCGCGUGUACCAUGAGU 480
Qy 481 GGCUCUUGCGCGUGUGCGCCACCGUGCAGCAGAUCCGCGACAGCGCGCAGCGCAGCCCA 540
Dy 481 GGAUUUUGCGCGUGUAUGUGCAACCUUGGNAACAGAUUGUGUACUCCCGCAUCGGUCUCA 540
Qy 541 CAGGCGAGUUGGUGACCAACCAACCCCGUGAUCAGGCGACGAGAACGAGAUUGGUGCGC 600
Dy 541 UAGGCAAAUUGGUGACCAACCAACCAACCAUUAUACAGACAUAGAGAACAGAAUGGUTU 600
Qy 601 CAGCACCGCGCCAGGCGCAGGAGCAGAUUGGCGCGCGCGCGCGCGCGCGCGCGCGAGGC 660
Dy 601 CAGCACUACAGCUGAAGGCGCAGGAGCAGAUUGGCGCGCGCGCGCGCGCGCGCGCGAGGC 660
Qy 661 CAUGGAGUGGCGCGCAGCGCCAGGCGCAGGAGUUGGCGCGCGCGCGCGCGCGCGCGCGC 720
Dy 661 CAUGGAGUUGGCGCGCAGGCGCAGGCGCAGGAGUUGGCGCGCGCGCGCGCGCGCGCGC 720
Qy 721 CCCCGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 780
Dy 721 UCCUAGCUCAGUGCGUGGUGUGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 780
Qy 781 GCGCAUGGCGCGCGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Dy 781 ACGAAUGGCGCGCGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Qy 841 CUCCCAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Dy 841 CUCCCAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Qy 901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
Dy 901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
```

```
RESULT 6
US-10-729-830-1
; Sequence 1, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: Optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
```



Db 661 ACTCACCTAGCTCAGTCCGGTCTAAAGATGATCTTTGAAATTTGCAGGCTAC 720  
Qy 776 CAGAAGCGCAUGGGCGUGCAGACGAGCGCUUCAAGUAAC 816  
Db 721 CAGAAACGGATGGGAGTGCAATGCAGGATTCAGGTGATC 761

## RESULT 8

US-10-177-390-31  
; Sequence 31, Application US/10177390  
; Publication No. US20030143743A1  
; GENERAL INFORMATION:  
; APPLICANT: Schuler, Gerold  
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear  
; TITLE OF INVENTION: Polynucleotides by Electroporation  
; FILE REFERENCE: 021505wo/JH/ml  
; CURRENT APPLICATION NUMBER: US/10/177,390  
; CURRENT FILING DATE: 2002-06-20  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: Influenza virus  
US-10-177-390-31

Query Match 52.0%; Score 489.4; DB 6; Length 1027;  
Best Local Similarity 65.2%; Pred. No. 5.6e-90;  
Matches 503; Conservative 92; Mismatches 176; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGAUAGCCUGCAGCGAGGUGGAGACCUACGUGUGAGCAUCAUCCCGAG 105  
Db 16 ATATTGAAAGATGAGTCTTAAACCGAGGTCGAAACGTACGTTCTCTATCATCCGTC 75  
Qy 106 CGGCCCCUUAAGCGCGAGUAGCCCGCAGAGCUGAGGACCGUUGUCCGCGCAAGCAC 165  
Db 76 AGGCCCCCTCAAGCCGAGATCGCACAGAGACTTGAAGATGCTTTGCAGGGAGAAACAC 135  
Qy 166 CGACUUGAGUGUGUGAGGUGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 225  
Db 136 CGATCTTGAGGTTCTATGGAATGGCTAAAGACAGACCAATCTGTCACTCTGACTAA 195  
Qy 226 GGGCAUCCUGGCUUUGUUGUACCCUGACCGGCGGAGGAGGAGGAGGAGGAGGAGGAG 285  
Db 196 GGGGATTTTAGGATTTGTGTTTCAAGCTCAGCGTCCCGTCCCGTCCCGTCCCGTCC 255  
Qy 286 CCGCUUCUGCAGACCGCCUGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 345  
Db 256 ACGCTTTGTCCAAATGCCCTTAAATGGGAAACGGGATCCAAATACATGGGCAAGCAGT 315  
Qy 346 GAAGCUGUACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 405  
Db 316 TAAACTGTATAGGAGCTCAGAGGGAGATTAACATTCATGGGCGCAAGAAATCTCACT 375  
Qy 406 GAGCUACAGCGCGCGCCUGGCGCAGCUGAGGCGGCGGAGGAGGAGGAGGAGGAGGAG 465  
Db 376 CAGTTATTCTGCTGCTGCACTTGCAGTTGTATGGGCTCATATACACAGGATGGGGC 435  
Qy 466 CGUACACCGAGGUGGCGUUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 525  
Db 436 TGTGACCACTGAAGTGGATTTGGCTTGTATGTGCAACCTGTGAACAGATTTGTGACTC 495  
Qy 526 CCAGCAGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 585  
Db 496 CCAGCATCGGTCTCATAGGCAATGGTGAACACACCAACCACTAATCAGACATGAGAA 555  
Qy 586 CAGGAUGGUGUGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 645  
Db 556 CAGAAATGGTTTATAGCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCGAGTGA 615  
Qy 646 CGAGGCCCGCGAGGCGCAUGGAGGUGGCGCAGCCAGCGCAGGCGAGGAGGAGGCGCAUGAG 705

Db 616 GCAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAATGGTCAAGGGATGAG 675  
Qy 706 GACCAUUGGACCCACCCAGCAGCAGCGCGCGCGGCGGAGGAGGAGGAGGAGGAGGAG 765  
Db 676 AACCATTTGGGACTCATCTAGCTCCAGTGTGCTGTGAAAAATGATCTTCTTGAATAATT 735  
Qy 766 GCAGGCGUACCAAGCGGCAUGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 816  
Db 736 GCAGGCGCTATCAGAAACGAATGGGGTGCAGATGCAACGGTTTCAAGTGATC 786

## RESULT 9

US-10-855-875-5  
; Sequence 5, Application US/10855875  
; Publication No. US20050003349A1  
; GENERAL INFORMATION:  
; APPLICANT: Kawakita, Yoshihiro  
; TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene T  
; FILE REFERENCE: 800.038US1  
; CURRENT APPLICATION NUMBER: US/10/855,875  
; CURRENT FILING DATE: 2004-05-27  
; PRIOR APPLICATION NUMBER: US 60/473,798  
; PRIOR FILING DATE: 2003-05-28  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: Influenza virus  
US-10-855-875-5

Query Match 51.8%; Score 487.8; DB 8; Length 1027;  
Best Local Similarity 64.6%; Pred. No. 1.2e-89;  
Matches 503; Conservative 94; Mismatches 182; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGAUAGCCUGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 105  
Db 16 ATATTGAAAGATGAGTCTTAAACCGAGGTCGAAACGTACGTTCTCTATCATCCGTC 75  
Qy 106 CGGCCCCUUAAGCGCGGAGUAGCCCGCAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 165  
Db 76 AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTTCTTTCAGGGAGAAACAC 135  
Qy 166 CGACUUGAGGUGUGAGGAGGUGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 225  
Db 136 CGATCTTTGAGGTTCTCATGGAATGGCTAAAGCAAGACCAATCTGTCTCTGACTAA 195  
Qy 226 GGGCAUCCUGGCGUUCGUGUUCACCCUGACCGGCGGAGGAGGAGGAGGAGGAGGAGGAG 285  
Db 196 GGGGATTTTAGGATTTGTGTTTCAAGCTCAGCGTCCCGTCCCGTCCCGTCCCGTCC 255  
Qy 286 CCGCUUCUGCAGACCGCCUGAGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 345  
Db 256 ACGCTTTGTCCAAATGCCCTTAAATGGGAAACGGGATCCAAATACATGGGCAAGCAGT 315  
Qy 346 GAAGCUGUACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 405  
Db 316 TAAACTGTATAGGAAAGCTCAAGAGGGAGATTAACATTCATGGGCGCGCAAGAAATCTCACT 375  
Qy 406 GAGCUACAGCGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 465  
Db 376 CAGTTATTCTGCTGCTGCACTTGGCCCTGTTATGGGCTCATATACACAGGATTTGTGACTC 435  
Qy 466 CGUACACCGAGGUGGCGUUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 525  
Db 436 TGTGACCACTGAAGTGGCAATTTGGCTTGTATGGGCTCATATACACAGGATTTGTGACTC 495  
Qy 526 CCAGCAGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 585  
Db 496 CCAGCATCGGTCTCATAGGCAATGGTGAACACACCAACCACTAATCAGACATGAGAA 555  
Qy 586 CAGGAUGGUGUGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 645  
Db 496 CCAGCATCGGTCTCATAGGCAATGGTGAACACCAACCACTAATCAGACATGAGAA 555  
Qy 586 CAGGAUGGUGUGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 645

Db 556 CAGAAATGGTTTATGACGAGCACTACAGCTTAAGGCTATGGAGCAAAATGGCTGGATCGATGGA 615  
Qy 646 GCAGGCGCCGAGGCGCAUGGAGGUGGCCAGCCAGGCGAGGAGUGGUGGCGGCAUGAG 705  
Db 616 GCAGCAGCAGAGGCGCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG 675  
Qy 706 GACCAUCCGACCCACCCAGCAGCAGCGCGGCCUGAAGAACGACCCUGGAGAACCU 765  
Db 676 AACCAATGGGACTCATCTAGCTCCAGTGCTGGTCTGAAATAATGATCTCTTGAAAAATTT 735  
Qy 766 GCAGGCUACCAAGAGCGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGG 824  
Db 736 GCAGGCGCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTTCAAGTGTATCTCTCACT 794

## RESULT 10

US-10-065-133A-1

; Sequence 1, Application US/10065133A  
; Publication No. US20030199074A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

; FILE REFERENCE: EQ-1-C2-1

; CURRENT APPLICATION NUMBER: US/10/065,133A

; PRIOR FILING DATE: 2002-12-10

; PRIOR APPLICATION NUMBER: PCT/US99/18583

; PRIOR FILING DATE: 1999-08-12

; PRIOR APPLICATION NUMBER: 09/133,921

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1023

; TYPE: DNA

; ORGANISM: Equine influenza virus H3N8

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (25)..(780)

; OTHER INFORMATION:

; FEATURE: misc feature

; NAME/KEY: (673)..(673)

; LOCATION: (673)..(673)

; OTHER INFORMATION: At nucleotide 673, r = a or g

; OTHER INFORMATION: At amino acid residue 213, Xaa = Val

US-10-065-133A-1

Query Match 51.7%; Score 487.4; DB 6; Length 1023;

Best Local Similarity 65.0%; Pred. No. 1.4e-89;

Matches 501; Conservative 93; Mismatches 177; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGAGGCGUGGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGG 105  
Db 15 ATATTAAAGATGAGTCTCTGACCGAGGTGCGAAACGTACGTTCTCTCTATCGTACCATC 74  
Qy 106 CGGCCCCUGAAGCGCGAGAGUGCCCGACAGGCGGACGACGUGUUCGCGCGGCAAGAACAC 165  
Db 75 AGGCCCCCTCAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTGCGGGAAGAACAC 134  
Qy 166 CGACGUGGAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 225  
Db 135 CGATCTTGAGGCACTCATGTAATGGCTAAGACAGACCAATCTGTCACTCTGACTAA 194  
Qy 226 GGGCAUCCUGGCGUUGUUGUACCCUGACCGGCGCCAGCGAGCGCGCGCGCGCGCGCGCG 285  
Db 195 AGGGATTTTAGGATTCGATTCACGCTCACCGTGCCAGTGCAGGAGGACTGCAGCGTAG 254  
Qy 286 CGCUUCCUGCAGACGCCUGAACCGCAACGGGACCCCAACACAGGACGAGGCGGU 345  
Db 255 ACGCTTTTGCCAAAATGCCCTTAGTGGAAACGGAGATCCAAACCAACATGGACAGAGCA 314  
Qy 346 GAAAGCUGUACAGGAAGCUGAAGAGGAGGAGUACACCUUCCACGCGCGCAAGGAGAGUACAGCCU 405

Db 315 AAAAATGTACAGGAAGCTTAAAAAGAGAAATAACATTCATCGGGCAAAAGAGGTGGCACT 374  
Qy 406 GAGCUACAGCGCCGCGCGCCUGGCGAGCUGCAUGGCGGCTUGAUCAACACGAGUGGCGC 465  
Db 375 CAGCTATTCCACTGCTGACCTAGCCAGCTGCTAGGGACTCATATACAAACAGATGGGAAC 434  
Qy 466 CGUACACCAACGAGGUGGCGUUCGCGCUGGUGGUGGCGCCACCCUGGAGCAGAUCCGCGCAG 525  
Db 435 TGTGACAAACGAGTGGCATTTGGCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494  
Qy 526 CCAGCACCGCAGCCAGGCGAGGUGGUGAACCACCAACCAACCCCGUGAUGGAGCGACGAGAA 585  
Db 495 CCAGCATCGATCTCACAGGCGAGATGGTGACAAACCAACCAACCAATTAATCAGACATGA 554  
Qy 586 CAGGAUGGUGGCGGCGAGCACCCAGCCAGGCGCAAGCGCAUGGAGGCGCGCGCGCAGCAGCA 645  
Db 555 CAGAAATGGTATTAGCCAGTACCACCGCTAAAGCCATGGAGCAGATGGCAGGCTGAGTGA 614  
Qy 646 GCAGGCGCGCGAGGCGCAUGGAGGUGGCGAGCGAGCGCGGCGAGGCGAGGCGCAUGAG 705  
Db 615 GCAGGCGAGCAGGCGCATGGAGGTTGCTAGTAAGGCTAGGCGAGATGTRCAGGCAATGAG 674  
Qy 706 GACCAUCCGACCCACCCAGCAGCAGCGCGCGCGUGAAGAACGACCCUGGAGAACCU 765  
Db 675 AACCAATGGGACCCACCCCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTCTTGAATAAT 734  
Qy 766 GCAGGCGUACCAAGAGGCGGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGG 816  
Db 735 GCAGGCGCTACCAAGAACCGATGGGAGTGCAGGATTCAGAGTATC 785

## RESULT 11

US-10-434-811A-1

; Sequence 1, Application US/10434811A

; Publication No. US20040022809A1

; GENERAL INFORMATION:

; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher

; APPLICANT: Education

; APPLICANT: Dowling, Patricia W.

; APPLICANT: Youngner, Julius S.

; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

; FILE REFERENCE: EQ-1-C1-PUS-1

; CURRENT APPLICATION NUMBER: US/10/434,811A

; CURRENT FILING DATE: 2003-05-08

; PRIOR APPLICATION NUMBER: PCT/US99/18583

; PRIOR FILING DATE: 1999-08-12

; PRIOR APPLICATION NUMBER: 09/133,921

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1023

; TYPE: DNA

; ORGANISM: Equine influenza virus H3N8

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (25)..(780)

; OTHER INFORMATION:

; NAME/KEY: misc feature

; LOCATION: (663)..(663)

; OTHER INFORMATION: At nucleotide 663, r = a or g

; OTHER INFORMATION: At amino acid residue 213, Xaa = Val

US-10-434-811A-1

Query Match

Best Local Similarity 51.7%; Score 487.4; DB 7; Length 1023;

Matches 501; Conservative 93; Mismatches 177; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGAGGCGUGGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGG 105  
Db 15 ATATTAAAGATGAGTCTCTGACCGAGGTGCGAAACGTACGTTCTCTCTATCGTACCATC 74



```
QY 106 CGGCCCCUGAGGCCGAGUVCGCCAGAGGCGUGGAGGAGUGUUCGCCGGCAAGAACAC 165
Db 75 AGGCCCCCTCAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTTCGAGGGGAAGAACAC 134
QY 166 CGACCUAGGUGUGUAGGUGGUGUAGAGACAGGCCCAUCCUGAGCCCCUGAGCAA 225
Db 135 CGATCTTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACTCTGACTAA 194
QY 226 GGGCAUCCUGGGCUUGUGUUCACCCUGACCGUGGCCAGGCGCGGCCUUCAGCGCCG 285
Db 195 AGGATTTTAGATTCTGATTTCAGCTCACCGTCCCGAGTGGAGCGAGGACTGCGAGCGTAG 254
QY 286 CCGCUUCUGUGAGAACCGCCUGAAGCGGAAACGGCGAACCCCAACAAUGAGCAAGGCGGU 345
Db 255 ACGCTTTGTCCAAATGCCCTTAGTGGAAACGGAGATCCAAACAAATGATGACAGAGCAGT 314
QY 346 GAAGCUUACAGGAGGAGGAGGAGAGUACCUUCCAGCGGCCAGGAGGAGUACGCCU 405
Db 315 AUAACCTGTACAGGAAGCTTAAAGAGAAATAACATTCCTATGGGCCAAAGAGGTGGCACT 374
QY 406 GAGCUACAGCGCCGCGCCCGGCGCAGCUGCAUGGGCGUGAUUACCAACAGGAGUGGCGCG 465
Db 375 CAGCTATTCACTGGTGCATAGCCAGCTGCATGGGACTCATATACACAGATGGGAAC 434
QY 466 CGUGACACCGAGGUGGCUUCGCGGUGGUGGUGGCGCCACCUUGCAGGAGUUCGCGACAG 525
Db 435 TGTGACAAACGGAAGTGGCATTTGGCTGGTATGGCGCACATGTGAACAGATCGCTGATTC 494
QY 526 CCAGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 585
Db 495 AACAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 554
QY 586 CAGGAUUGGUGUGGCGGAGCAGCCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 645
Db 555 CAGAAATGGTATTAGCCAGTACCACCGCTAAAGCCATGGAGCAGATGGCGGGTCGAGTGA 614
QY 646 GCAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 705
Db 615 GCAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 674
QY 706 GACCAUUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 765
Db 675 AACCATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 734
```

RESULT 12  
US-10-734-373-1

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; LOCATION: (25) .. (780)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (673) .. (673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-734-373-1

Query Match 51.7%; Score 487.4; DB 7; Length 1023;
Best Local Similarity 65.0%; Pred. No. 1.4e-89;
Matches 501; Conservative 93; Mismatches 177; Indels 0; Gaps 0;

QY 46 AGAUUUAAGAUAGAGCCUGCUGACCCAGAGGCGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 105
Db 15 ATATTTAAAGATGAGTCTTTCTGACCGAGGTGCAACGTAAGTCTCTTATCTGATACCATC 74
QY 106 CGGCCCCUGAGGCCGAGUVCGCCAGAGGCGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 165
Db 75 AGGCCCCCTCAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTTCGAGGGGAAGAACAC 134
QY 166 CGACCUAGGUGUGUAGGUGGUGUAGAGACAGGCCCAUCCUGAGCCCCUGAGCAA 225
Db 135 CGATCTTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACTCTGACTAA 194
QY 226 GGGCAUCCUGGGCUUGUGUUCACCCUGACCGUGGCCAGGCGCGGCCUUCAGCGCCG 285
Db 195 AGGATTTTAGATTCTGATTTCAGCTCACCGTCCCGAGTGGAGCGAGGACTGCGAGCGTAG 254
QY 286 CCGCUUCUGUGAGAACCGCCUGAAGCGGAAACGGCGAACCCCAACAAUGAGCAAGGCGGU 345
Db 255 ACGCTTTGTCCAAATGCCCTTAGTGGAAACGGAGATCCAAACAAATGATGACAGAGCAGT 314
QY 346 GAAGCUUACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 405
Db 315 AUAACCTGTACAGGAAGCTTAAAGAGAAATAACATTCCTATGGGCCAAAGAGGTGGCACT 374
QY 406 GAGCUACAGCGCCGCGCCCGGCGCAGCUGCAUGGGCGUGAUUACCAACAGGAGUGGCGCG 465
Db 375 CAGCTATTCACTGGTGCATAGCCAGCTGCATGGGACTCATATACACAGATGGGAAC 434
QY 466 CGUGACACCGAGGUGGCUUCGCGGUGGUGGUGGCGCCACCUUGCAGGAGUUCGCGACAG 525
Db 435 TGTGACAAACGGAAGTGGCATTTGGCTGGTATGGCGCACATGTGAACAGATCGCTGATTC 494
QY 526 CCAGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 585
Db 495 AACAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 554
QY 586 CAGGAUUGGUGUGGCGGAGCAGCCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 645
Db 555 CAGAAATGGTATTAGCCAGTACCACCGCTAAAGCCATGGAGCAGATGGCGGGTCGAGTGA 614
QY 646 GCAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 705
Db 615 GCAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 674
QY 706 GACCAUUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 765
Db 675 AACCATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 734
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RESULT 13  
US-10-872-014-1  
; Sequence 1, Application US/10872014  
; Publication No. US20040234553A1  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of  
; APPLICANT: Dowling, Patricia W.  
; Higher Ed



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Qy 466 CGUGACCAACCGAGGUGGCGCUUGCGGUGUGCGCCACUUGCGAGCAGAUCCGCCAGAG 525
Db 435 TGTGACAACCGAAGTGGCATTTGGCCTTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494
Qy 526 CCAGCACCGGACCCACAGGAGUGGAGUAGCACCACCAACCCCGGCUAGUACAGGACAGAGAA 585
Db 495 CCAGCATCGATCTCACAGGCGAGATGGTGACATTAACCAACCCATTAATCAGACATGAAGA 554
Qy 586 CAGGAUGGUGUGCGCCAGCAGCACCACCGCAAGGCCAUGGAGCAGAUCCGCCGCGCAGCAGGA 645
Db 555 CAGAATGGTATTAGCCAGTACCAACCGCTTAAGCCATGGAGCAGATGGCAGGGTCCAGTGA 614
Qy 646 GCAGGCCGCGAGGCGGAGGUGGCGCAGCGCCAGCAGGCGCAGAGUGGAGGCGCAUGAG 705
Db 615 GCAGGCGAGCAGAGGCCCATGGAGGTGTCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674
Qy 706 GACCAUCGCGACCCACCCAGCAGCAGCGCGGCGUGAAGAAACGACUUGUGGAGAGAACCU 765
Db 675 AACCATTTGGGACCCACCCCTAGCTCCAGTGCCTGGTTGAAAGATGATCTCTCTTGAATTT 734
Qy 766 GCAGGCCUACAGAAAGCGCAUGGCGGUGCGAGUAGCAGCGCUUCAAAGUGAAC 816
Db 735 GCAGGCCCTACAGAAACGGATGGGAGTGCAAAATGCAGCGATTCAAGTGATC 785

RESULT 15
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EO-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-434-811A-4

Query Match 51.4%; Score 484.6; DB 7; Length 1023;
Best Local Similarity 64.9%; Pred. NO. 5.3e-89;
Matches 500; Conservative 92; Mismatches 179; Indels 0; Gaps 0;

Qy 46 AGAUCAAAGAUGAGCGUGAGCCGAGGUGGAGACCUAGCGUGAGCAUCAUCCGCCAG 105
Db 15 ATATTTAAAGATGATGCTTCTGACCGAGGTGGAACGTACGTTCTCTATCTTACCATC 74
Qy 106 CGGCCCCCGUAGGCGGAGUAGCGCCAGAGGCGUGGAGGACGUGUUGCGCGGCAAGAACAC 165
Db 75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTGGCAGGGAAGAACAC 134
Qy 166 CGACUUGAGGUGUGUAGGAGGUGGCUAAGACCCAGGCCCAUCCUAGCGCCCGUAGCCAA 225
Db 135 CGATCTTGAGGCACCTCATGGAAATGGCTAAAGACAAGACCAATCTGTCTGACTGATAA 194
Qy 226 GGGCAUCCUGGCGUUGUUCACCCUGACCGUGGCGAGCGAGCGCGCGCCUGCAGCGCGG 285
Db 195 AGGGATTTTAGGATTCGTATTACGCTCACCGTGCCAGTGAGCGGAGGACTGCGAGGTAG 254
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Qy 286 CCGCUUGUGCAGAAACGCCUGAACCGCAACGCGACCCCAACCAACAUAGGAGGCGCGU 345
Db 255 ACCCTTTTGTCCAAAATGCCCTTGTAGTGAACCGGAGATCCAAACAACTATGACAGAGCAGT 314
Qy 346 GAAGCUGUACAGGAAGCUGAAGAGGAGAGUACUUCUCCAGCGGCCCAAGAGAGAUACGCCU 405
Db 315 AANACTGTACAGGAAGCTTAAAGAGAGAAATAACATTCATGGGGCAAAAGAGGTGGCACT 374
Qy 406 GAGCUCACAGCGCGCGCGCCCGGCGCAGCAGCUGCAGUAGGCGCUUACUACAAACAGGAUGGCGC 465
Db 375 CAGCTATTCCACTTGGTGCACCTAGCCAGCTGCTGGGACTCATATACAACAGAAATGGGAAC 434
Qy 466 CGUGACCAACCGAGGUGGCGCUUCGCGCCUGUGUGCGCCACCUGCGAGCAGAUCCGCCAGAG 525
Db 435 TGTGACAACCGAAGTGGCATTTGGCCTTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494
Qy 526 CCAGCACCGCAGCCACAGCAGAGUAGUAGCACCACCAACCCCGUAGUACAGGACAGGAGAA 585
Db 495 CCAGCATCGATCTCACAGGCGAGATGGTGACATAACCAACCCATTAATCAGACATGAAGA 554
Qy 586 CAGGAUGGUGUGCGCGCAGCAGCACCACCGCAAGGCCAUGGAGCAGAUCCGCCGCGCAGCAGGA 645
Db 555 CAGAATGGTATTAGCCAGTACCAACCGCTAAAGCCATGGAGCAGATGGCAGCGGTCCAGTGA 614
Qy 646 GCAGGCCGCGGAGGCGGCGGCGCAGCGCCAGCAGGCGCAGAGUAGGCGCAUGAG 705
Db 615 GCAGGCGAGCAGAGGCCCATGGAGGTGTCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAG 674
Qy 706 GACCAUCGCGACCCACCCAGCAGCAGCGCGCGCGUAGAAACGACUUGUGGAGAGAACCU 765
Db 675 AACCATTTGGGACCCACCCCTAGCTCCAGTGCCTGGTTGAAAGATGATCTCTCTTGAATTT 734
Qy 766 GCAGGCCUACAGAAAGCGCAGUAGGCGGUGCGAGUAGCAGCGCUUCAAAGUGAAC 816
Db 735 GCAGGCCCTACAGAAACGGATGGGAGTGCAAAATGCAGCGATTCAAGTGATC 785
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Search completed: March 21, 2006, 13:38:09  
Job time : 927.936 secs









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RESULT 5
US-11-131-479-79
; Sequence 79, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Optimized M1 Coding Region
US-11-131-479-79

Query Match      70.9%; Score 667.8; DB 12; Length 759;
Best Local Similarity 80.6%; Pred. No. 9.4e-70;
Matches 612; Conservative 90; Mismatches 57; Indels 0; Gaps 0;

Qy 56 AUGAGCCUGACCGGAGGUGGAGACCUAUCGUGUGAGCAUCCCGAGCGGCCCGCUG 115
Db 1 ATGAGCTGCTGACCGAGGTCGAAAGTATGTTCTCTATCGTCCCGAGCGGCCCTG 60

Qy 116 AAGCCCGAGAUCCCGAGGUGGAGGAGCGUGUUGCGCGGCAAGAACACCGACUGAG 175
Db 61 AAGCCCGAGATCGCCAGAGACTGGAGGACGTGTTGCGCGGCAAGAACACCGACCTGAG 120

Qy 176 GUGCUGAUGGAGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 235
Db 121 GCCCTGATGGAGTGGCTGAAGACACGACCCATCTGTAGCCCTGTGACCAAGGGATCCTG 180

Qy 236 GGUUUGUGUACCCUGACCGUGCCAGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 295
Db 181 GGCTTCGTGTTTCACTGACCGTGCCTGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240

Qy 296 CAGAACCGCCUGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 355
Db 241 CAGAACCGCTTGAAGAGAGATCACCTTCCACGCGGCGGAGGAGGAGGAGGAGGAGGAGGAG 300

Qy 356 AGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 415
Db 301 AGAAGAGTGAAGAGAGATCACCTTCCACGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360

Qy 416 GCCGCGCGCCUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 475
Db 361 GCCGCGCGCCUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420

Qy 476 GAGUGGCGCUUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 535
Db 421 GAGGTGGCTTTCGGGCTGGTGGCGCACTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480

Qy 536 AGCCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 595
Db 481 AGCCACAGAGAGTGGTGGGCGACCAACCCCTGTATCAGACAGGAGGAGGAGGAGGAGGAG 540

Qy 596 CUGGCCAGACCAACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 655
Db 541 CTGGCCAGACCAACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600

Qy 556 GAGGCCAUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 715
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Db 601 GAGCCATGGAGATGCCAGCGGCGGAGACAGATGGTGCGGCCATGAGAGCCATCGGC 660
Qy 716 ACCACCCCGAGCAGCAGCGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 775
Db 661 ACCACCCCGAGCAGCAGCGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Qy 776 CAGAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 814
Db 721 CAGAAACGAATGGGGGTGCAGATGCAACGATCAAGTGA 759

RESULT 6
US-11-131-479-28
; Sequence 28, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-28

Query Match      63.4%; Score 597.6; DB 12; Length 756;
Best Local Similarity 75.0%; Pred. No. 1.3e-61;
Matches 567; Conservative 90; Mismatches 99; Indels 0; Gaps 0;

Qy 56 AUGAGCCUGACCGGAGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 115
Db 1 ATGAGTCTGCTGACAGAGGTTGAGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60

Qy 116 AAGCCCGAGAUCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 175
Db 61 AAGCCCGAGATTCGCCAGAGACTGGAGGAGCTTTCGCCCGGCAAGAACACCGATCTGGAG 120

Qy 176 GUGCUGAUGGAGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 235
Db 121 GTGCTGATGAGTGGCTGAAGACTGCGCCCATCTGTCTCCCTGACAAAGGGCATCCTG 180

Qy 236 GGUUUGUGUACCCUGACCGUGCCAGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 295
Db 181 GGCTTCGTATTACTACTGACCGTCCCTCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240

Qy 296 CAGAACCGCCUGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 355
Db 241 CAGAACCGCTTGAAGCGGCAAGCGGATCCCAACATGATGAAGGCGGTGAAGCTGTAT 300

Qy 356 AGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 415
Db 301 AGAAGCTGAAGCGAGAGATCACATTTATGGCGCAAGGAGATATCGCTGAGCTACAGT 360

Qy 416 GCAGGCGCCUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 475
Db 361 GCAGGCGCCUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420

Qy 476 GAGUGGCGCUUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 535
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Db 421 GAGGTAGCCTTTGGCCTGCTGGCCCACTTGGCAGCAGATCGCGCACTCTCAGCATAGA 480
Qy 536 AGCCACGCGAGUGGUGGACACCAACCAACCCUUGAUCAGCGCAGAGAAAGGAGUGUG 595
Db 481 TCTCAGACAGATGGTGACGACTCAAAACCCCTTGATACGGCAGAGACAGGATGGT 540
Qy 596 CUGGCCAGCACACCAGCCCAAGGCCCAUGGAGCAGAGUGGCCGCGCAGCAGCGCCGCC 655
Db 541 CTGGCCTCTACTACCGCCCAAGGCCATGGAGCAGATGGCGCGCAGCAGTGAGCGCGCC 600
Qy 656 GAGGCAUGGAGUGGCGCAGCCAGCCAGCGCAGAGUGGUGGAGGCAACCAUAGCGC 715
Db 601 GAGGCCATGGAGGTAGCTCTCAGGCCAGCGCAGCGAGATGGTGCAGGCCATCGCAACCATCGGC 660
Qy 716 ACCACCCAGCAGCAGCGCGCGCCUGAAGAACGACCGUGGAGAACCGUGCAGCGCUAC 775
Db 661 ACTCACCCCTCAGCTCTGCGGCCCTGAAGAACGACCTGCTGGAGAACCTCGAGGCCCTAT 720
Qy 776 CAGAACGCGAUGGGCGUGCAGAGCAGCGCUUCAG 811
Db 721 CAGAGAGAAATGGCGGTACAGATGCAGAGGTTTCAAG 756

RESULT 7
US-11-131-479-26
; Sequence 26, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-26

Query Match 52.1%; Score 491; DB 12; Length 756;
Best Local Similarity 66.2%; Pred. No. 3e-49; Mismatches 165; Indels 0; Gaps 0;
Matches 500; Conservative 90;

Qy 56 AUGACCGUGUACCGAGGUGGAGACCUAGCGUGGAGCAUCAUCCCGCAGCGGCCCGUG 115
Db 1 ATGAGCTTGCTAAACAGAGTGGAAACCTATGCTCTCATATCATCTTCTAGCGGCCCTTA 60

Qy 116 AAGCCGAGUAGCGCCAGCGGUGGAGCAGCGUGUUGCGCGCAAGAACACCGACGUGAG 175
Db 61 AAAGCCGAATCGCTCAGCGGCTCAGGAGTGTGTTTGGCGGCAAGAACACCGACCTGGAG 120

Qy 176 GUGCUGAGGAGUGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 235
Db 121 GTATTGATGGAGTGGCTGAAACCGGACCTATTTCTGAGCGCCCTGACTAAGGGAACTACT 180

Qy 236 GCGUUGUGUUCACCGUACCGUGCCAGCGAGCGCGCGCGUGCAGCGCGCGCGCGUUCUG 295
Db 181 GCGTTGTTTTAGATTGACCGTGGCCCTCAGAGAGGGGTCTCCAAAGAGGAGGGCTTCGTG 240

Qy 296 CAGAACCGCCUAGACGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 355
Db 241 CAGAACCGCTTAAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCG 300
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Qy 356 AGAAGCUGAAGAGGAGAUCAUCCUACCGCGCCCAAGGAGAUCAUCCUGAGCUACAGC 415
Db 301 CGCAATTAAGCGGAGATAACCTTCCATGGAGCCAAGGAGATCTCCCTGTCTTACTCT 360
Qy 416 GCGCGCGCCUGGCGCAGCUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 475
Db 361 GCAGGTCTCTCGCTGCTGATGGGACTTATCTACAAACCGAATGGCGGCGGCGGCTCAACA 420
Qy 476 GAGGUGGCGUUCGCGGUGGUGCGCCACCGGCGGAGAGUAGCGCGGAGCAGCAGCAGCGC 535
Db 421 GAAGTGCTTTTCGGGCTGGGTGGCAACTTTCGCAACAGATGCTGACAGTCAGCAGCGG 480
Qy 536 AGCCACAGGAGAGUGGUGACCAACCAACCCCGAUCAGCGCAGAGAAAGGAGUGUG 595
Db 481 TCCACCGCTCAATGGTCACCAACCAATCCGCTGATTAGACATGAAATCGCATGGT 540
Qy 596 CUGGCCAGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 655
Db 541 CTAGCATCAACTACAGCCAAAGCAATGGAAACAAATGGCGGAGACTCCGAGCAGGCTGCC 600
Qy 656 GAGGCCAUGGAGUGGCGCAGCGCAGCGCAGAGUAGGUGGAGGAGGAGGAGGAGGAGGAG 715
Db 601 GAGCGATGGAGGTGGCGTCCCGCAGCGCAGAGATGGTACAGGCTATGAGAACTATCGGT 660
Qy 716 ACCCAGCCAGCAGCAGCGCGCGGCGGCGGAGAAACCGCUGGAGAGAACCGUGCAGCGCUAC 775
Db 661 ACGCACCAAGTTCTTCAGCTGGGCTGAAGAAATGATCTTCTTGAGAACCTGCGAGGCTAC 720
Qy 776 CAGAACGCGAUGGGCGUGCAGAGCAGCGCUUCAA 810
Db 721 CAAAAGCGGATGGCGCTCCAGATGCAGAGATTTAA 755

RESULT 8
US-11-131-479-3
; Sequence 3, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza A virus
US-11-131-479-3

Query Match 51.4%; Score 484.6; DB 12; Length 1027;
Best Local Similarity 64.9%; Pred. No. 1.6e-48;
Matches 500; Conservative 92; Mismatches 179; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGUAGCGUGGAGCGGCGGAGAGACCUAGCGUGGAGAGAACCGUGAGCAUCCCCAG 105
Db 16 ATATTGAAGATGATGTTCTTAACCGAGGTGCGAAACGTACTCTCTATCATCCCCGTC 75

Qy 106 CGGCCCCUGAAGCGCGGAGAUCCGCGCAGAGCGGAGAGCGUGUUCGCGCGCAAGAACAC 165
Db 76 AGGCCCCCTCAAGCCAGATCGCACAGAGACTTGAAGATGTCTTTGCGAGGAGAGACAC 135

Qy 166 CGACCGGAGUGGUGGAGGUGGAGAGACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 225
Db 166 CGACCGGAGUGGUGGAGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 225
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 987
; TYPE: DNA
; ORGANISM: human Influenza A virus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(987)
; OTHER INFORMATION: human Influenza A virus
; OTHER INFORMATION: strain A/Charlottesville/31/95 (H1N1)
; OTHER INFORMATION: accession number af398876
US-11-155-478A-131

```

| Query Match           | 49.2%           | Score 463.4  | DB 12    | Length 987 |
|-----------------------|-----------------|--|----------|------------|
| Best Local Similarity | 63.9%           | Pred. No. 4.6e-46  |          |            |
| Matches 486           | Conservative 89 | Mismatches 186   | Indels 0 | Gaps 0     |
| Qy                    | 56              | AUGAGCCUGUGACCCGAGGUGGAGACCUACUGCUGUGAGCAUCCCCAGCGGCCCCUG        | 115      |            |
| Db                    | 1               | ATGAGTCTTTCTAACCGAGGTGAAACGTACGTTCTCTATCGTCCGTGAGGCCCTC          | 60       |            |
| Qy                    | 116             | AAGCCGAGAUCCGCCAGAGCGUGGAGACGUGUUCGCGCCAGAGAACACCGACUGGAG        | 175      |            |
| Db                    | 61              | AAAGCCGAGATCGCACAGAGACTTGAAGATGCTCTTGTCTGGAAGAAACACCGATCTTGAG    | 120      |            |
| Qy                    | 176             | GUGCUGAGGAGUGGUGNAGACAGCGCCCAUCCUGAGCCGCCUGACCAAGGGCAUCCUG       | 235      |            |
| Db                    | 121             | GCTCTCATGGAGTGGCTAAAGCAAGACCGATCTCTGCTCCTCTGACTAAGGGGATTTTA      | 180      |            |
| Qy                    | 236             | GGCUUCUGUUAACCCUGACCGUGGCCAGCGAGCGCGGCCUGCAGCGCGCGGUUCUG         | 295      |            |
| Db                    | 181             | GGATTTGTGTTACGCTCACCGTGCCTGCCAGTGCAGCGAGGACTGCAGCGTGTGTC         | 240      |            |
| Qy                    | 296             | CAGAACGCCUGAAGCGGCAACGGCGACCCCAACAAUGGACAGGCCGUGAAGGCUAC         | 355      |            |
| Db                    | 241             | CAAAATGCCCTTAAATGGGAAATGGGGATTCCAAATAACATGGAACAGAGCAGTTAAATCTGAT | 300      |            |
| Qy                    | 356             | AGGAAGCUGAAGAGGGAGUACACCUCCACGGCGCCCAAGGAGAUACGCCUGCAGCUACAGC    | 415      |            |
| Db                    | 301             | AGAAGCTTAAGAGGGAGATTAACATTCATGGGGCCAAAGAAATAGCACTCAGTTATCT       | 360      |            |
| Qy                    | 416             | GCGCGGCCCTUGGCGAGCUGCAUGGGGCCUGAUCAACACAGGAUGGGCGCGUGACCA        | 475      |            |
| Db                    | 361             | GCTGGTGCACCTTGCAGTTGTATGGGCTTCATATACAACAGATGGGGCTGTGACCA         | 420      |            |
| Qy                    | 476             | GAGGUGGCCUUCGGCCUGGUGCGCCACCUUGCAGCGAGCAUGCGCGACAGCCGAC          | 535      |            |
| Db                    | 421             | GAATCAGCATTTGGCCCTGATATGGCCAACTGTGAACAGATTTGCTGACTCCCGACAT       | 480      |            |
| Qy                    | 536             | AGCCACAGGAGUGGUGACCAACCAACCCUUGAUCAGGCACGAGAACAGGAUGGUG          | 595      |            |
| Db                    | 481             | TCTCNTAGGCNAATGGTTAAACAAACCAATCCATTAATAGACATAGAACAGATGGTT        | 540      |            |
| Qy                    | 596             | CUGGCCAGCACACCGCCAGGCCCAUGGAGCAGAUUGGCCGCGCAGCAGCGCGCC           | 655      |            |
| Db                    | 541             | CTGGCCAGCACTACAGCTAAAGCTATGGAGCAATGGCTGGATCGAGTGAACAGAGCAG       | 600      |            |
| Qy                    | 656             | GAGGCCAUGGAGUGGCCAGCCAGGCAGGAGUGGUGCAGGCGCCUAGAGAACCAUCCGC       | 715      |            |
| Db                    | 601             | GAGGCCATGAGGTTGTAGTTCAGGCAGGCAAAATGGTGCAGGCAATGAGAGCCATTGGG      | 660      |            |
| Qy                    | 716             | ACCCACCCACGACGACGCGCGGCCUGAAGAACCAACCCUGCUGGAGAACCUUGAGGCCUAC    | 775      |            |
| Db                    | 661             | ACTCATCTAGCTTAGCACTGGTCTGAATAATGATCTTCTTGAATAATTTGCAGGCC         | 720      |            |
| Qy                    | 776             | CAGAAGCGCAUGGGCGUGCAGUAGCGCGCUUCAAAGUAGAC                        | 816      |            |
| Db                    | 721             | CAGAAACGAATGGGGGTGCATATGCAACGATTTCAAGTGATC                       | 761      |            |

RESULT 11  
US-11-131-479-95  
; Sequence 95, Application US/11131479

```

; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4756 RV-Sali into VR10682 RV
; US-11-131-479-95

```

| Query Match           | 48.5%           | Score 457.6  | DB 12    | Length 4822 |
|-----------------------|-----------------|--|----------|-------------|
| Best Local Similarity | 62.1%           | Pred. No. 1.6e-45  |          |             |
| Matches 487           | Conservative 93 | Mismatches 204   | Indels 0 | Gaps 0      |
| Qy                    | 33              | GCUCAUCUUGGCAGAUCAUAAAGAUAGAGCCUGUGACCGAGGUGGAGACCUACGUGCUGA   | 92       |             |
| Db                    | 791             | GATCAGATATCGAATTCGCCACCATGAGCTTTTAAACGAGGTCGAACATGATGTTCTCT    | 850      |             |
| Qy                    | 93              | GCAUCAUCCCAAGCCGCCCCUGAAGCCGAGAUCCGCCAGAGGUGGAGGACGUGUUCG      | 152      |             |
| Db                    | 851             | CTATCGTTCATCAGGCCCCCTCAAAGCCGAAATCGGCAGAGACTTGAAGATGCTCTTG     | 910      |             |
| Qy                    | 153             | CCGGCAAGAACAACCGACGUGGAGGUGUGAGUGGCGUGAAGACAGAGCCCCNACUGA      | 213      |             |
| Db                    | 911             | CTGGGAAAAACACAGATCTTTGAGGCTCTCATGGAATGGCTTAAAGACAAGACCAATCCTGT | 970      |             |
| Qy                    | 213             | GCCCCUGACCAAGGCAUCCUGGGCUUCUGUUAACCCUGACCGUCCGAGCGAGCGCG       | 272      |             |
| Db                    | 971             | CACCTCTGACTAAGGGATTTTGGGTTTGTTGTTTACGCTCACGTCGCCAGTGAGCGAG     | 1030     |             |
| Qy                    | 273             | GCUCGAGCCGCGCGCUUCUGUCAGAAACGCCCCUGAACGGCAACGGCGACCCCAACAACA   | 332      |             |
| Db                    | 1031            | GACTGCAGCGTAGACGCTTTGTCCAAAATGCCCTCAATGGGNAATGGGATCCAAATAACA   | 1090     |             |
| Qy                    | 333             | UGGACAAGGCCGUGAAGCUGUUA CAGGAAGCUGAAGAGGGAGAUCAACUUCACGCGGCCA  | 393      |             |
| Db                    | 1091            | TGGCAGAGCAGTTAAACTATATAGAAAACTTAAGAGGGAGATTACATTCATGGGGCCA     | 1150     |             |
| Qy                    | 393             | AGGAGUACGCCUGAGCUACAGCGCGCGGCCCCUGGCCACGUCGCAUGGGCGCAUACUA     | 452      |             |
| Db                    | 1151            | AAGAAATAGCACTCAGTTATTCTGCTGGTGCACTTGCCAGTTGCATGGGCCTCATATACA   | 1210     |             |
| Qy                    | 453             | ACAGGAGUGGCGCGUGACACCGAGGUGGCCUUCGCGCCUGUGUGCGCCACACUGCGAGC    | 512      |             |
| Db                    | 1211            | ACGAATGGGGGTGTAAACCACTGAATGGCTTTGGCCCTGGTATGTGCAACATGTGAAC     | 1270     |             |
| Qy                    | 513             | AGAUCCCGACGCCACGACCGCGACAGGCGAGGAGUGUGAACAACAACCCCCUGA         | 572      |             |
| Db                    | 1271            | AGATTGTGACTCCAGCACAGGTCTCATAGGCAAAATGGTGGCAACAACCAATCCATTAA    | 1330     |             |
| Qy                    | 573             | UCAGGCACGAGAACGAGUUGUCUGGCCACGACCCACCGCCAGGCGCAUGGAGCAGUUG     | 632      |             |
| Db                    | 1331            | TAAGGCATGAGAACAGAAATGGTTTGGCCACGACTACAGCTAAGGCTATGGAGCAATGG    | 1390     |             |
| Qy                    | 633             | CCGCGACGACGAGCAGGCGCGGAGCCCAUGAGGUGGCGACGCGAGGCGCAGGCAUUG      | 692      |             |
| Db                    | 1391            | CTGATCAAGTAGCAGGCGAGCGGCGCCATGGAATTTGCTAGTTCAGCCGACGCAATGG     | 1450     |             |
| Qy                    | 693             | UGCAGGCCAUGAGGACCAUCGCGACCCACCCACGACGACGCGCGCCUGAAGAACGACC     | 752      |             |



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Qy 273 GCUUGCAGCGCGCGCUUUGUGCAGACGCGCCUGAACGGCAACGGGACCCCAACA 332
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
6505 GACTGACGCTAGACGCTTTGTCCTCAATGCGCTCAATGGGAATGGGGATCCAAATAACA 6446
Qy 333 UGGAACAGCGCGUGAGCUGUACAGGAAGAGUGAAGAGAGAGAGAUCAACCUUCCACGGCGCA 392
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
6445 TGGACAGACGAGTTAAACTATATAGAAAATCTTAAGAGGGAGATTACATTCCATGGGGCA 6386
Qy 393 AGGAGUACGUGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 452
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
6385 AAGAAATAGCACTCAGTTATTCTGCTGTGTGCACTTGGCAGATTGCAATGGGCGCTCATATA 6326
Qy 453 ACAGAUAGGGCGCGUGACCAACCGAGUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 512
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
6325 ACAGAAATGGGGCTGTAACTGAGTGGCTTTGGGCTGTGTGCAACATGTGAC 6266
Qy 513 AGAUGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 572
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6265 AGATTGCTGACTCCAGCAGCAGGCTCTCATAGGCAAAATGGTGGCAACCAACCAATCCATTAA 6206
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Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
6205 TAAGGCATGAGAACAGAAATGGTTTGGCGCAGCACTACAGCTAAGGCTATGGAGCAAAATGG 6146
Qy 633 CGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 692
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6145 CTGATCAAGTGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 6086
Qy 693 UGAGGCGUAGAGGACCAUCCGCGCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 752
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
6085 TGCAGGCAATGAGAGCCTATGGGACTCATCTCAGTCTGCTGCTCTAAAGATGATC 6026
Qy 753 UGUUGAGAACCUAGCAGCCTUACAGAGCGCAUGGCGUGGCGUGGCGUGGCGUGGCGUGGCG 812
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6025 TTCTTGAATAATTCAGACCTTATCAGAAACGAATGGGGGTGCAGATGCAACGATTCAGT 5966
Qy 813 GAAC 816
Db 5965 GACC 5962
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## RESULT 14

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US-11-131-479-60
; Sequence 60, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for Fragment 7 from VR4756
US-11-131-479-60
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Query Match 48.5%; Score 457; DB 12; Length 982;  
Best Local Similarity 63.2%; Pred. No. 2.6e-45;  
Matches 481; Conservative 90; Mismatches 190; Indels 0; Gaps 0;

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1 ATGAGCCTTCTAAACCGAGGTCGAAAAGTATGTTCTCTATCGTTCCATCAGGCGCCCTC 60
Qy 116 AAGCCCGAGAUCCGCGCAGGCGUGGAGAGCGUUGUUCGCGCAAGACACCGAGCUGAG 175
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61 AAAGCCGAAATCGCGCAGAGACTTTGAAGATGTCTTTGCTGGGAAAAACACAGATCTTGAG 120
Qy 176 GUGCUGAUGAGUGGCGUAGAAGCAGGCGCCCAUCCUGAGCCCGCGUGACCAAGGGAUCCUG 235
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121 GCTCTCATGAAATGGCTTAAGACAAAGACCAATCTCTGTCACTCTGACTAAGGGATTTTG 180
Qy 236 GGUUUGUGUUCACCCUGACCGUGCCAGGAGCGCGCGCGUGCAGCGCGCGCGCGCGUGUG 295
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 GGGTTTGTGTTCAAGCTCAACCGTGCAGTGAGCGAGGACTGACGCGTAGACGCTTTGTC 240
Qy 296 CAGAACCCCGUGAAGGCGCAACGGCGACCCCAACAAACAAUGACAAAGGCGGUGAAGCUGUAC 355
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
241 CAAATGCCCTCAATGGGGAATGGGGATCCAAATTAACATGGAACAGAGCAGTTAAACTATAT 300
Qy 356 AGGAAGCUGAAGAGGAGAUCAACCUUGCAACGGCGCCAAAGGAGAUCAAGCUGAGCUACAGC 415
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 AGAAAATCTTAAGAGGAGATTAATTCATGGGGCCAAAGAAATAGCACTCAGTTATTCT 360
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361 GCTGTTGCACTTGGCAGTTGATGGGCTCATATACAAAGAAATGGGGCTGTAACCACT 420
Qy 476 GAGUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 535
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
421 GAAGTGGCGCTTTGGCGCTGGTATGTGCAACATGTGAACAGATTTGCTGACTCCAGCAGCAG 480
Qy 536 AGCCACAGGCGAGUGGAGCACCACCAACCCCGUGAUCAGGCGCAGGACGAGAGUUGUG 595
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481 TCTCATAGGCAATGGTGGCAACCAATCCATTAATAGGCATGAGAACAGATGGTT 540
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Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
541 TTGGCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCAAGTGAGCAGGACCG 600
Qy 656 GAGGCCAUGAGUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 715
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601 GAGGCCATGGAATTTGCTAGTCAGGCCAGGCAATGGTGGCAGCAATGAGAGCCATTGGG 660
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661 ACTCATCTAGCTCCAGTGTGGTCTAAAGATGATCTCTTGAATAATTTGCAGACCTAT 720
Qy 776 CAGAAGCGCGAGUGGCGUGCAGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 816
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721 CAGAAACGAATGGGGGTGCAGATGCAACGATTCAGGTGACC 761
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## RESULT 15

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US-11-131-479-101
; Sequence 101, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101
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Run on: March 20, 2006, 23:02:13 ; Search time 204.984 Seconds  
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Title: US-10-729-830-7  
Perfect score: 1011  
Sequence: 1 gcugucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaaaa 1011

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 479.6 | 47.4        | 4023   | 3     | US-08-809-513A-8   |
| 2          | 479.6 | 47.4        | 4802   | 3     | US-08-809-513A-6   |
| 3          | 477.6 | 47.2        | 1023   | 3     | US-09-506-286B-1   |
| 4          | 477.6 | 47.2        | 1023   | 3     | US-09-762-861B-1   |
| 5          | 477.6 | 47.2        | 1023   | 3     | US-10-065-133A-1   |
| 6          | 477.6 | 47.2        | 1023   | 3     | US-10-434-811A-1   |
| 7          | 477.4 | 47.2        | 816    | 3     | US-09-311-784A-13  |
| 8          | 474.8 | 47.0        | 1023   | 3     | US-09-506-286B-4   |
| 9          | 474.8 | 47.0        | 1023   | 3     | US-09-762-861B-4   |
| 10         | 474.8 | 47.0        | 1023   | 3     | US-10-065-133A-4   |
| 11         | 474.8 | 47.0        | 1023   | 3     | US-10-434-811A-4   |
| 12         | 474.2 | 46.9        | 756    | 3     | US-09-506-286B-3   |
| 13         | 474.2 | 46.9        | 756    | 3     | US-09-762-861B-3   |
| 14         | 474.2 | 46.9        | 756    | 3     | US-10-065-133A-3   |
| 15         | 474.2 | 46.9        | 756    | 3     | US-10-434-811A-3   |
| 16         | 471.4 | 46.6        | 756    | 3     | US-09-506-286B-6   |
| 17         | 471.4 | 46.6        | 756    | 3     | US-09-762-861B-6   |
| 18         | 471.4 | 46.6        | 756    | 3     | US-10-065-133A-6   |
| 19         | 471.4 | 46.6        | 756    | 3     | US-10-434-811A-6   |
| 20         | 465.2 | 46.0        | 1027   | 6     | PCT-US95-12357A-3  |
| 21         | 79.4  | 7.9         | 290    | 3     | US-10-131-827-8418 |
| 22         | 79.4  | 7.9         | 1069   | 3     | US-09-372-422A-7   |
| 23         | 79.4  | 7.9         | 1387   | 3     | US-09-475-515-34   |
| 24         | 79.4  | 7.9         | 1944   | 3     | US-09-475-515-37   |

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| 25 | 79.4 | 7.9 | 1944 | 3 | US-09-475-515-38  | Sequence 38, Appl |
| 26 | 79.4 | 7.9 | 1944 | 3 | US-09-475-515-40  | Sequence 40, Appl |
| 27 | 79.4 | 7.9 | 1944 | 3 | US-09-475-515-43  | Sequence 43, Appl |
| 28 | 79.4 | 7.9 | 1944 | 3 | US-09-475-515-46  | Sequence 46, Appl |
| 29 | 79.4 | 7.9 | 2466 | 3 | US-09-475-515-49  | Sequence 49, Appl |
| 30 | 79.4 | 7.9 | 4608 | 3 | US-09-475-515-76  | Sequence 76, Appl |
| 31 | 79.2 | 7.8 | 2403 | 2 | US-08-471-033-30  | Sequence 30, Appl |
| 32 | 79.2 | 7.8 | 2403 | 2 | US-08-471-044-30  | Sequence 30, Appl |
| 33 | 79.2 | 7.8 | 2403 | 2 | US-08-463-483A-30 | Sequence 30, Appl |
| 34 | 79.2 | 7.8 | 2403 | 2 | US-08-471-046A-30 | Sequence 30, Appl |
| 35 | 79.2 | 7.8 | 2403 | 2 | US-08-470-566B-30 | Sequence 30, Appl |
| 36 | 79.2 | 7.8 | 2403 | 2 | US-08-838-219B-7  | Sequence 7, Appl  |
| 37 | 79.2 | 7.8 | 2403 | 2 | US-08-469-334-30  | Sequence 30, Appl |
| 38 | 79.2 | 7.8 | 2403 | 3 | US-09-300-529-30  | Sequence 30, Appl |
| 39 | 79.2 | 7.8 | 2403 | 3 | US-09-233-336A-7  | Sequence 7, Appl  |
| 40 | 79.2 | 7.8 | 2403 | 3 | US-09-233-752A-7  | Sequence 7, Appl  |
| 41 | 79.2 | 7.8 | 2403 | 3 | US-09-402-036-7   | Sequence 7, Appl  |
| 42 | 79.2 | 7.8 | 2403 | 3 | US-09-904-226-7   | Sequence 7, Appl  |
| 43 | 77.6 | 7.7 | 1097 | 3 | US-09-832-129-21  | Sequence 21, Appl |
| 44 | 77.6 | 7.7 | 2241 | 2 | US-08-838-219B-20 | Sequence 20, Appl |
| 45 | 77.6 | 7.7 | 2241 | 3 | US-09-233-336A-20 | Sequence 20, Appl |

ALIGNMENTS

RESULT 1  
US-08-809-513A-8  
; Sequence 8, Application US/08809513A  
; Patent No. 6524588  
; GENERAL INFORMATION:  
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette  
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a  
; TITLE OF INVENTION: Method  
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS  
; STREET: 660 White Plains Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591-5144  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage  
; COMPUTER: Gateway Pentium II  
; OPERATING SYSTEM: Windows 98  
; SOFTWARE: Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,513A  
; FILING DATE: 24-MAR-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/03663  
; FILING DATE: 18-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94115505.3  
; FILING DATE: 30-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurt G. Briscoe  
; REGISTRATION NUMBER: 33,141  
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 332-1700  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4023 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO

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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus, RNA sequence
; INDIVIDUAL ISOLATE: pHL1490
US-08-809-513A-8

Query Match 47.4%; Score 479.6; DB 3; Length 4023;
Best Local Similarity 65.2%; Pred. No. 7.2e-72;
Matches 494; Conservative 90; Mismatches 174; Indels 0; Gaps 0;

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201 TTTGTGTTTCAGCTCACCGTCCAGTGAGGAGAGACTGACGCTAGACGTTTGTCAA 260
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261 AATGCCCTTAATGGGAACGGGGATCCAAATAAATGAGCAAGCAGTTAAACTGTATAGG 320
Qy 428 AAGCUGAAGAGGAGAGACUACUUCACGGCCGCAAGGAGAUACGCGUAGCAAGCGCC 487
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
321 AAGCTCAAGAGGAGATAACTATCCATGGGGCCAAAGAAATCTCACTCAGTTATCTGCT 380
Qy 488 GCGCCCGUGGACGUGCAUGGCGUGAUCAACAGAGUUGGCGCGUGACCAACCGAG 547
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381 GGTGCACTTGCCAGTTGTATGGGCTCATATACACAGAGTGGGGCTGTGACCACTGAA 440
Qy 548 GUGGCGCUUGGCGUGUGGCGCCACCGUGAGCAGAUUGCGCAGCAGCACCGCAGC 607
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441 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATGCTGACTCCAGCATCGGTCT 500
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Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
501 CATAGGCAAAATGGTGACAAACCAACCAACCACTAATACAGACATGAGAACAGAAATGTTTA 560
Qy 668 GCCAGCACCGCCAGGCGCAUGGAGCAGAUUGGCGGCGAGCAGCGAGCGCCGAG 727
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561 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGATCGAGTGAAGAGAGAGAG 620
Qy 728 GCCAUGGAGGUGGCGCAGCCAGGCGCAGAUUGGUGAGGCGCAUGAGGACCAUCCGCA 787
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
621 GCCATGGAGGTTGCTAGTCAGGCTAGGCAATGGTGAAGCGATGAGAACCATTTGGGACT 680
Qy 788 CACCCAGCAGCAGCGCCGCGUGAAGAACACGUGUGGAGAACUCCAGCGCCUACAG 847
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681 CATCTAGCTCCAGTGGTGTGAAAAAATGCTCTTTGAAAAATTTTCAGGCGCTATCAG 740
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741 AAACGATGGGGGTGCAGATGCAACCGGTTCAAGTATC 778
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RESULT 2
US-08-809-513A-6
; Sequence 6, Application US/08809513A
; Patent No. 652458
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
```

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Gateway Pentium II
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,513A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03663
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94115505.3
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6802 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus, RNA sequence
; INDIVIDUAL ISOLATE: pHL1191
US-08-809-513A-6
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Query Match 47.4%; Score 479.6; DB 3; Length 6802;
Best Local Similarity 65.2%; Pred. No. 7.7e-72;
Matches 494; Conservative 90; Mismatches 174; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGGAGACUAGUGUGAGCAUCCAGCGGCCGCCCUAGAAG 187
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41 AGTCTTCAACCGAGGTGGAACGTACTCTCTATCATCCGTAGGCCCCCTCAA 100
Qy 188 GCCGAGAUCCGCCAGAGCGUGAGGACGUGUUCGCCGCAAGAACACCGACCGUGAGUG 247
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 GCCGAGATCGCACAGAGACTTGAAGATGCTCTTCGAGGAAGAACACCGATCTTGAGGTT 160
Qy 248 CUGAUGAGUGGUGUAGAGACAGGCCCAUCCUGAGCCCUAGCAAGGGCAUCCUGGCC 307
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
161 CTCATGGAATGGGTAAAGACAAAGACCAATCTCTGACTGAAAGGGGATTTTAGGA 220
Qy 308 UUCGUGUACCGUACCGUGGCCAGCGAGCGGCGCGUGAGCGGCCCGCGUUGUGCAG 367
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
221 TTTGTGTTTCAGCTCACCGTCCAGTGAGGAGAGACTGACGCTAGACGTTTGTCAA 280
Qy 368 AACGCCCUAGCGCAACCGCGACCCCAACAAACAUUGGACAAAGGCCGUGUAGCAGG 427
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281 AATGCCCTTAATGGGAACGGGGATCCAAATAAATGAGCAAGCAGTTAAACTGTATAGG 340
Qy 428 AAGCUGAAGAGGAGAGAUACUUCACCGCGGCCCAAGGAGAUACGCGUAGCAGGCC 487
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
341 AAGCTCAAGAGGAGAGATAAATTCATGGGGGCCAAAGAAATCTCACTCAGTTATCTGCT 400
Qy 488 GCGCCCGUGGCGCAGUGGCGGCGUAGCAACAGAGUUGGCGCGUGACCAACCGAG 547
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 401 GGTGCACTTGGCAGTTGTATGGGCTCATATACAAAGAGATGGGGCTGTGACCACTGAA 460  
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Db 461 GTGGCAITTTGGCTGTGTATGTGCAACCTGTGACAGATTTGCTGACTCCAGCATCGTCT 520  
Qy 608 CACAGGAGAGUGGAGACCAACCAACCCUUGAUCAAGGACGAGAAACAGGAGUGUGUG 667  
Db 521 CATAGGCAAAATGGTGACAAACCAACCAACCACTAATCAGACATGAGAACAGAAATGTTT 580  
Qy 668 GCCAGCACCGCCAGGCGCAUGAGCAGAGAUUGGCGCGCAGCAGGAGCGCGCGAG 727  
Db 581 GCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGATCGAGTGAGCAGAGAGAG 640  
Qy 728 GCCAUGGAGUGGCGCAGCGCCAGGCGAGGAGUGGAGGCGCAUGAGCAACCAUGCGCAC 787  
Db 641 GCCATGGAGGTTGTATGTCAGGCTAGGCAATGTGTGAGCGATGAGAACCTTTGGACT 700  
Qy 788 CACCCAGCAGCAGCGCGCGCUGAAGAACGACCUUGUGGAGAACCUUGAGCGCCUACCCAG 847  
Db 701 CATCTAGCTCCAGTGTGTGTGAAATAATGCTCTCTTTGAAATTTGCGAGGCTATCAG 760  
Qy 848 AAGCGCAUGGCGUGCAGAUUGCAGCGCGCUUCAAAGUGAAC 885  
Db 761 AAACGAATGGGGTGCAGATGCAACGGTTCAAGTGATC 798

RESULT 3

US-09-506-286B-1  
; Sequence 1, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; APPLICANT: The University of Pittsburgh, of the Commonwealth  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; PRIOR FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION: At location 663, r = A or G; At amino acid  
; OTHER INFORMATION: location 213, Xaa = Val  
US-09-506-286B-1

Query Match 47.2%; Score 477.6; DB 3; Length 1023;  
Best Local Similarity 65.0%; Fred. No. 1.3e-71;  
Matches 493; Conservative 90; Mismatches 175; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGGAGUGGAGACCUACGUGUGAGCAUCCCGCAGCGCGCCUGAAG 187  
Db 28 AGTCTTCTGACGAGGTGCAACGTAAGTCTTCTCTATCTGTAACATCAGGCGCCCTCAA 87  
Qy 188 GCCGAGUVCGCCGAGGUGGAGGAGCGUGUUGCGCGCAAGAACACCGACCGUGAGUG 247  
Db 88 GCCGAGATCGCGCAGAGACTTGAAGATGCTTTGCGAGGAAGAACACCGCATCTTTAGGCA 147  
Qy 248 CUGAUGGAGUGGCTUGAAGACAGCGCCCAUCCUGAGCCCGCUGACCAAGGGCAUCCUGGC 307  
Db 148 CTCATGGAATGGCTAAAGACAAGAACCAATCTCTGTCTGACTTAAGAGGATTTTAGGA 207  
Qy 308 UUCGUGUACCCUGACCGUGGCCCGCAGCGCGCGCUGCAGCGCGCGCGUGUGCAG 367

Db 208 TTGCTATTCACTGCTCACCGTCCAGTGAGCGAGGACTGCAGCGGTAGACGCTTTGTCAA 267  
Qy 368 AACGCCUGAAGCGGACCGGACCCCAACCAUUGGAGAACGCCUGAGGAGCUUACAGG 427  
Db 268 AATGCCCTTATGTGAAACCGGAGATCCAAACAAATGAGCAGAGCAGGTAAACTGTACAGG 327  
Qy 428 AAGCUGAAGAGGAGAUCAACUCCACGCGCGCCAAAGAGAGAUCAAGCCUGAGCUACAGGCC 487  
Db 328 AAGCTTAAAGAGAAATAACATTTCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387  
Qy 488 GGGCCCGUGCGCAGCUGCAUGGCGCUUACUACAAAGAGUUGGCGCGCGUGACCAACCGAG 547  
Db 388 GGTGCACTAGCCAGCTGATGGGACTCATATACAACAGAAATGGGAACCTGTGACAAACGAA 447  
Qy 548 GUGGCCUUGCGCGUGUGCGCCACCGUGGAGCAGAUUGCGCGCACACCGCAGCACCAGC 607  
Db 448 GTGCAATTTGGCTGTGTATGGCCACATGTGAAACAGATCGCTGATTTCCAGCATCTGATCT 507  
Qy 608 CACAGGAGAGUGGACCAACCAACCCUUGAUGGAGCGCAGGACGAGAAACAGAGUGUGUG 667  
Db 508 CACAGGAGATGTTGACAAACCAACCCATTAAATCAGACATGAANAACAGAAATGTTATTA 567  
Qy 668 GCCAGCACCAACCGCAAGGCGAUGGAGCAGAUUGGCGCGCAGCAGCGAGCGCGCGAG 727  
Db 568 GCCAGTACCACCGCTAAAGCCATGGAGCAGATGGCAGGGTCTGAGTGAGCGGACGAG 627  
Qy 728 GCCAUGGAGUGGCGCAGCGCGCAGCAGAUUGGAGCGCAUGGAGCGCAAGCGGACCGCACC 787  
Db 628 GCCATGGAGTTTGTAGTAAGGCTTAGGCAGATGTRCAGGCAATGAGAACCATTTGGGACC 687  
Qy 788 CACCCAGCAGCAGCGCGCGCGCAGAACGACCUUGUGAGAACCUUGCAGGCGCUACAG 847  
Db 688 CACCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTTGAANAATTTGACAGGCGCTACCAG 747  
Qy 848 AAGCGCAUGGCGUGGAGUAGUGCGCGCUUCAAAGUGAAC 885  
Db 748 AAACGATGGGAGTGCAAAATGCAGCGATTCAAGTGATC 785

RESULT 4

US-09-762-861B-1  
; Sequence 1, Application US/09762861B  
; Patent No. 6579528  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS (formerly HK2-033CPUS)  
; CURRENT APPLICATION NUMBER: US/09/762,861B  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(780)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (673)..(673)  
; OTHER INFORMATION: At nucleotide 673, r = a or g  
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val  
US-09-762-861B-1

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Query Match 47.2%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 65.0%; Pred. No. 1.3e-71;
Matches 493; Conservative 90; Mismatches 175; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGGAGACCUAGUGUGAGCAUACUCCAGCGGCCCGCCUGAAG 187
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
28 AGTCTTCTGACCGAGGTGGAACGTAGCTTCTCTATCGTACCATAGGCCCGCCCTCAA 87
Qy 188 GCCGAGAUCCCGCAGGUGGAGGAGCGUUGUCCCGGCAAGAACACCGCUGGAGUG 247
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
88 GCCGAGATCGCGAGAGACTTGAAGTCTCTTCGAGGAGAGACACCGATCTTGAGGCA 147
Qy 248 CUGAUGAGUGGUGAAGACAGCGCCCAUCCUGAGCCCGCCUGACCAAGGGGCAUCCUGGGC 307
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148 CTCATGGAATGGCTTAAGACAGACCAATCTCTCTATCGTACCATAGGCCCGCCCTCAA 207
Qy 308 UUCGUGUACCCUGACCGUGCCCGAGCGCGCCUGCAGCGCCCGCGCCUGUGCAG 367
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208 TTGCTATTTCAGCTCACCGTCCCGAGTGAGGAGACTGCGAGCGTAGACGCTTTGTCAA 267
Qy 368 AACCCCGCUGAACCGGCAACCGCGACCCCAACCAACUAGGACAGGCGCGUGAAGCUACAGG 427
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268 AATGCCCTTAGTGGAAACGAGATCCAAACAACTGACAGAGCAGTAAACTGTACAGG 327
Qy 428 AAGCUGAAGAGGGAGAUACCUUCCAGCGCGCCAGGAGAUACGCCUGAGCUACAGCGCC 487
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 AAGCTTAAAGAGAAATAACATTCATGGGGCAAGAGGTGGCACTCAGCTATTCCACT 387
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388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAGAAATGGGAACCTGTGACAAACGAA 447
Qy 548 GUGCGCUUCCUGGUGCGCCACUGCGAGCAGAUCCGCGCAGCCAGCCAGCCGCGAGC 607
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448 GTGGCATTTGGCTTAAAGCCTAAGGCTAGGAGAGTGGGCTGATTCACGATCGATCT 507
Qy 608 CACAGGCGAUGUGUACCAACCAACCGCCCGCUGAUCAGGACGAGAAACAGAAUGUGUG 667
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508 CACAGGCGAGATGGTGAACCAACCCATTAATGAGATGATCTCTTGAATAATTTGAGG 727
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Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
628 GCCATGAGGTTGCTAGTAAAGCTAGGAGAGTGGAGAGTGGAGAGGAGGAGGAGGAG 687
Qy 788 CACCCAGCAGCAGCGCGCGCGUGAAGAACCAACUGUGGAGAACCUUGCAGGCGCUACAG 847
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688 CACCCAGCAGCAGCGCGCGCGUGAAGAACCAACUGUGGAGAACCUUGCAGGCGCUACAG 747
Qy 848 AAGCGCAUGGCGUGCAGUACGCGGCUUACAGUAGAAC 885
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
748 AAGCGGATGGAGTGCAATGCGAGGATTCAGGATGATC 785
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## RESULT 5

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US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
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; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, xaa = Val
US-10-065-133A-1
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Query Match 47.2%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 65.0%; Pred. No. 1.3e-71;
Matches 493; Conservative 90; Mismatches 175; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGGAGACCUAGUGUGAGCAUACUCCAGCGGCCCGCCUGAAG 187
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
28 AGTCTTCTGACCGAGGTGGAACGTAGCTTCTCTATCGTACCATAGGCCCGCCCTCAA 87
Qy 188 GCCGAGAUCCCGCAGGUGGAGGAGCGUUGUCCCGGCAAGAACACCGCUGGAGUG 247
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
88 GCCGAGATCGCGAGAGACTTGAAGTCTCTTCGAGGAGAGACACCGATCTTGAGGCA 147
Qy 248 CUGAUGAGUGGUGAAGACAGCGCCCAUCCUGAGCCCGCCUGAAGCGGCGUGAAGCUACAGG 307
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
148 CTCATGGAATGGCTTAAGACAGACCAATCTCTCTATCGTACCATAGGCCCGCCCTCAA 207
Qy 308 UUCGUGUACCCUGACCGUGCCCGAGCGCGCCUGCAGCGCCCGCGCCUGUGCAG 367
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208 TTGCTATTTCAGCTCACCGTCCCGAGTGAGGAGACTGCGAGCGTAGACGCTTTGTCAA 267
Qy 368 AACCCCGCUGAACCGGCAACCGCGACCCCAACCAACUAGGACAGGCGCGUGAAGCUACAGG 427
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
268 AATGCCCTTAGTGGAAACGAGATCCAAACAACTGACAGAGCAGTAAACTGTACAGG 327
Qy 428 AAGCUGAAGAGGGAGAUACCUUCCAGCGCGCCAGGAGAUACGCCUGAGCUACAGCGCC 487
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 AAGCTTAAAGAGAAATAACATTCATGGGGCAAGAGGTGGCACTCAGCTATTCCACT 387
Qy 488 GGCGCCUGGCGACUGCAUGGCGGCGUACUACACAGGAGGCGCGGCGUGACCAACCGAG 547
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388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAGAAATGGGAACCTGTGACAAACGAA 447
Qy 548 GUGCGCUUCCUGGUGCGCCACUGCGAGCAGAUCCGCGCAGCCAGCCAGCCGCGAGC 607
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
448 GTGGCATTTGGCTTAAAGCCTAAGGCTAGGAGAGTGGGCTGATTCACGATCGATCT 507
Qy 608 CACAGGCGAUGUGUACCAACCAACCGCCCGCUGAUCAGGACGAGAAACAGAAUGUGUG 667
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508 CACAGGCGAGATGGTGAACCAACCCATTAATGAGATGATCTCTTGAATAATTTGAGG 727
Qy 728 GCCATGAGGTTGCTAGTAAAGCTAGGAGAGTGGAGAGTGGAGAGGAGGAGGAGGAG 787
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628 GCCATGAGGTTGCTAGTAAAGCTAGGAGAGTGGAGAGTGGAGAGGAGGAGGAGGAG 687
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688 CACCCAGCAGCAGCGCGCGCGUGAAGAACCAACUGUGGAGAACCUUGCAGGCGCUACAG 747
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748 AAGCGGATGGAGTGCAATGCGAGGATTCAGGATGATC 785
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Db 748 AAACGGATGGAGTGCATAATGCAGCGATTCAAGTGATC 785
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Youngner, Patricia W.
; APPLICANT: Dowling, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-434-811A-4
Query Match 47.0%; Score 474.8; DB 3; Length 1023;
Best Local Similarity 64.9%; Pred. No. 3.8e-71;
Matches 492; Conservative 89; Mismatches 177; Indels 0; Gaps 0;
Qy 128 AGCCUGUGACCGGAGGAGGAGACCUACGUGUGAGCAUACUCCAGGGGCCCCCUAGAAG 187
Db 28 AGTCTTCTGACCGAGGTGCAACAGTACGTTCTCTCTATCTTACCATCAGGCCCCCTCAA 87
Qy 188 GCCGAGAUCCGACGAGGCGGAGGAGGUGUUCGCGGCAAGACACACCGACCUAGGAGUG 247
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Qy 248 CUGAUGGAGUGGCGUGAAGACAGGCGCCCAUCCUGAGCCCCUGACCAAGGGCAUCCUGGC 307
Db 148 CTCATGGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAAAGGGATTTAGGA 207
Qy 308 UUCGUGUACCCUGACCGUGCCGACGAGCGCGGCGUGAGCGCGCGCGCGCGCGCGUGUG 367
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Qy 548 GUGGCCUUCGCGGUGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 607
Db 448 GTGGATTTGGCCCTGTGATGCGCCACATGTGAACAGATCGCTGATTTCCACATCGATCT 507
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US-09-506-286B-3
; Sequence 3, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-3
Query Match 46.9%; Score 474.2; DB 3; Length 756;
Best Local Similarity 65.1%; Pred. No. 4.7e-71;
Matches 490; Conservative 89; Mismatches 174; Indels 0; Gaps 0;
Qy 128 AGCCUGUGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 187
Db 4 AGTCTTCTGACCGAGGTGCAACAGTACGTTCTCTCTATCTGATACCATCAGGCCCCCTCAA 63
Qy 188 GCCGAGAUCCGACGAGGCGGAGGAGGUGUUCGCGGCAAGACACCGACCUAGGAGUG 247
Db 64 GCCGAGATCGCGAGAGACTTGAAGATGTCTTTGAGGGAAGAACCGATCTTGAGCA 123
Qy 248 CUGAUGGAGUGGCGUGAAGACAGGCGCCCAUCCUGAGCCCCUGACCAAGGGCAUCCUGGC 307
Db 124 CTCATGGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAAAGGGATTTAGGA 183
Qy 308 UUCGUGUACCCUGACCGUGCGGAGGCGCGGCGUGAGCGCGCGCGCGCGCGCGUGUG 367
Db 184 TTCGTATTTCACGCTCACCGTGCACGAGTGTGAGCGGAGGACTGCGAGCGTGTGTCNA 243
Qy 368 AACGCCUGAAGCGGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 427
Db 244 AATGCCCTTAGTGAAACGAGATCTCAAACAACTGGACAGACAGTAAACTGTACAGG 303
Qy 428 AAGCTGAAGAGGGAGAUACCUCCACGCGCGCCCAAGGAGAUACGACGUGACUACAGGCC 487
Db 304 AAGCTTAAAGAGAAATAACATTTCATGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363
Qy 488 GGCGCCUGGCGAGGUGGCGGCGUGAUCAUACAGGAGUGGCGCGCGGCGCGGCGGAG 547
Db 364 GGTGCACTAGCGAGTGTGAGGAGTCTATATACAAAGATGGGAATGTGTACAAACCGAA 423
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Db 424 GTGGCAATTGGCTGTGATGGCCACATGTGAACAGATCGTGTATCCAGCATCGATCT 483  
Qy 608 CACAGGAGAGUGGUGACCAACCAACCCUUGAUGAGCGACGAGAACAGGAGUGUG 667  
Db 484 CACAGGAGAGTGTGACAAACCAACCCATTAATCAGACATGAACAGAAATGATATTA 543  
Qy 668 GCCAGCACACCGCCCAAGGCGAUGGAGCAGAGUGGCGGCGAGCAGCAGCGCCCGAG 727  
Db 544 GCCAGTACACCGCTAAAGCCATGGAGCAGATGGCAGGTCGAGTGAGCAGGCGAGAG 603  
Qy 728 GCCAUGGAGUGGCGCAGCGCCAGGCGAGGAGUGGAGGCGAUGAGGACCAUUGGCGACC 787  
Db 604 GCCATGGAGGTTGCTAGTAAGGCTAGGCGAGATGCTRCAGGCAATGAGAACCAATTGGGACC 663  
Qy 788 CACCCACGACGACGCGCGCGCUGAAGAACGACGACGUGGAGAACGUGGAGAACGUGGAG 847  
Db 664 CACCCAGTCTCAGTGGCGGTTTGAAGATGATCTCTTGAATAATTTGACGGCTTACCG 723  
Qy 848 AAGCGCAUGGCGUGAGCAGGCGCGUUCUACG 880  
Db 724 AACCGATGGGAGTGCAAAATGACGCGATTCAAG 756

## RESULT 13

US-09-762-861B-3  
; Sequence 3, Application US/09762861B  
; Patent No. 6579528  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-CL-PUS (formerly HKZ-033CPUS)  
; CURRENT APPLICATION NUMBER: US/09/762,861B  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-09-762-861B-3

Query Match 46.9%; Score 474.2; DB 3; Length 756;  
Best Local Similarity 65.1%; Pred. No. 4.7e-71;  
Matches 490; Conservative 89; Mismatches 174; Indels 0; Gaps 0;  
Qy 128 AGCCUGUGACCGAGGUGGAGACCUAGUGUGAGCAUACUCCCGCGCCCGCCUGAAG 187  
Db 4 AGTCTTCTGACCGAGGTCGAAACGTAACGTTCTCTCTATCGTACCATCAGGCGCCCTCAA 63  
Qy 188 GCCGAGUACCGCCAGGCGCCCAUCCUGAGCCCGCCGACCAACCGGCGGCGGCGG 247  
Db 64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTTCAGGGAAGAACACCGGATCTTGAGGCA 123  
Qy 248 CUGAUGGAGUGGCGUAGAACGACGCGCCCAUCCUGAGCCCGCCUGACCAAGGCGAUCUGGGC 307  
Db 124 CTCATGGATGGCTTAAGACAAGACCAATCTCTGTACCTCTGACTTAAGGATTTTAGGA 183  
Qy 308 UUCGUGUACCCUGACCGGCGCCAGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGG 367  
Db 184 TTCGTATTACGCTCACCGTCCCGAGTGGAGGAGGAGTGCAGCGTAGACGCTTTGTCAA 243  
Qy 368 AACGCGUAGACGGCAACCGGCGACCCCAACAAUGAAGCAAGGCGGCGGCGGCGGCGG 427  
Db 244 AATGCCCTTAGTGGAAACGGAGATCCAAACAACTGGAAGAGGATGAACTGTACAGG 303

Qy 428 AAGCUGAAGAGGGAGAUACUCCUCCAGCGCGCCAAAGGAGAUACUCCUGAGCUACAGCGCC 487  
Db 304 AAGCTTAAAGAGAAAATAACATTCATGGGCAAAAGAGGTGGCACATCAGCTATTCCACT 363  
Qy 488 GGCGCCUGGCGAGCUCGAGGCGUGAUCUACAAAGGAGUGGCGGCGGCGGCGGCGG 547  
Db 364 GGTGCACTAGCGAGCTGATGGGACTCATATATACACAGAAATGGGAACCTGTACAAACCGAA 423  
Qy 548 GUGGCGUUGGCGUGUGCGCCACUUGCGAGCAGAUCCGCGAGCAGCGACGACGACCGCAGC 607  
Db 424 GTGGCATTTGGCTTGGTATGGCCACATGTGAACAGATCGTGTATCCAGCATCGATCT 483  
Qy 608 CACAGGAGAGUGGAGCAACACCAACCCCGUGAUGAGGCGACGAGAACAGAGUGUGUG 667  
Db 484 CACAGGAGATGGTGACAAACCAACCAACCCATTATATGACATGAACAGAAATGATATTA 543  
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Qy 728 GCCAUGGAGUGGCGCAGCGCGAGGCGAGGCGAGGCGGCGGCGGCGGCGGCGGCGG 787  
Db 604 GCCATGAGGTTGCTAGTAAGGCTAGGCGATGATGTRCAGGCAATGAGAACCATTTGGGACC 663  
Qy 788 CACCCAGCAGCAGCGCGCGCGCGUAGAACGACGACGUGGAGAACGUGGAGAACGUGGAG 847  
Db 664 CACCCAGTCTCAGTGGCGGTTTGAAGATGATCTCTCTTGAATAATTTGACGGCTTACCG 723  
Qy 848 AAGCGCAUGGCGUGAGCAGGCGCGUUCUACG 880  
Db 724 AACCGATGGGAGTGCAAAATGACGCGATTCAAG 756

## RESULT 14

US-10-065-133A-3  
; Sequence 3, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-3

Query Match 46.9%; Score 474.2; DB 3; Length 756;  
Best Local Similarity 65.1%; Pred. No. 4.7e-71;  
Matches 490; Conservative 89; Mismatches 174; Indels 0; Gaps 0;  
Qy 128 AGCCUGUGACCGAGGUGGAGACCUAGUGUGAGCAUACUCCCGCGCCCGCCUGAAG 187  
Db 4 AGTCTTCTGACCGAGGTCGAAACGTAACGTTCTCTCTATCGTACCATCAGGCGCCCTCAA 63  
Qy 188 GCCGAGUACCGCCAGGCGCCCAUCCUGAGCCCGCCGACCAACCGGCGGCGGCGG 247  
Db 64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTTCAGGGAAGAACACCGGATCTTGAGGCA 123  
Qy 248 CUGAUGGAGUGGCGUAGAACGACGCGCCCAUCCUGAGCCCGCCUGACCAAGGCGAUCUGGGC 307  
Db 124 CTCATGGATGGCTTAAGACAAGACCAATCTCTGTACCTCTGACTTAAGGATTTTAGGA 183  
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Qy      428  AAGCUGAAGAGGAGAUCAACUUCACGCGCCGCAAGGAGAUCAAGCUGAGGCUACAGCGCC 487
Db      304  AAGCTTAAAGAGAAATAACATTCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363
Qy      488  GGCGCCUUGGCGGCGUGAUCGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 547
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Qy      548  GUGGCGUUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 607
Db      424  GTGGCAATTTGGCTGGATGCGGCACATGTGAACAGATCGTGTATCCAGCATCGATCT 483
Qy      608  CACAGGCGAGUUGGUGACACCAACCAACCCUUGAUCAGGCGACGAGAAACAGAGUUGUGUG 667
Db      484  CACAGGCGAGTGGTGACAAACCAACCAACCAATTAATCAGACATGAAACAGAAATGGTATTA 543
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Db      544  GCCAGTACCAAGCGGCTAAAGCCATGGAGCAGATGGCGGTGCGTGTGAAGATGATCTCCTTGA 603
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Db      604  GCCATGGAGGTGTAGTAAGCTAGGCGAGTGTGTCAGGCAATGAGAACCAATTTGGGAGCC 663
Qy      788  CACCCCGACAGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 847
Db      664  CACCCCTAGCTCAGTGGCGGTTTGAAGATGATCTCCTTGAAGATGATCTCCTTGAAGATGATCT 723
Qy      848  AAGCGCAUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 880
Db      724  AAACGGATGGGAGTGCAATGCAGCGATTCAAG 756
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## RESULT 15

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; Sequence 3, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-434-811A-3
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Query Match 46.9%; Score 474.2; DB 3; Length 756;
Best Local Similarity 65.1%; Pred. No. 4.7e-71;
Matches 490; Conservative 89; Mismatches 174; Indels 0; Gaps 0;
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Qy      128  AGCCUGUGACCGGAGGAGAGACCUACGUGUGAGAGCAUCCCGGCGGCGGCGGCGGCGGCGGCGG 187
Db      4   AGTCTTCGACCGAGGTGCAACGTCAGCTTCTCTATCGTACCATCATGAGGCGGCGGCGGCGG 63
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Qy      248  CUGAUGAGUGGCGUGAAGACACGAGCGCCCAUCUGAGGCGCCCGGCAAGGCGCAUCCUGGGC 307
Db      124  CTATGGATGGCTAAAGACAAGCAACCACTCTCTACCTCTGACTAAGGATTTTAGGA 183
Qy      308  UUGGUGUACACCGUGACCGUGCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367
Db      184  TTGCTATTACGCTCACCGTCCAGTGAGGAGGACTGCGAGCGGTAGACGCTTTGTCAA 243
Qy      368  AAGCGCCUGAAGCGGCAACGCGGACCCCAACAAUAGGACAAAGGCGGCGGUGAGGCUACAGG 427
Db      244  AATGCCCTTAGTGGAAACGGAGATCCAAACCAATGGACAGAGCAGTAAACCTGTACAGG 303
Qy      428  AAGCUGAAGAGGAGAUCAACUUCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487
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Db      364  GGTGCACTAGCAGCTGCTGATGGGACTCATATACAAAGATGGGAACTGTGACAAACGAA 423
Qy      548  GUGGCGUUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 607
Db      424  GTGGCAATTTGGCTGGATGCGGCACATGTGAACAGATCGCTGATTTCCAGCATCGATCT 483
Qy      608  CACAGGCGAGUUGUGACCAACCAACCCUUGAUCAGGCGACGAGAAACAGAGUUGUGUGUG 667
Db      484  CACAGGCGAGTGGTGACAAACCAACCAACCAATTAATCAGACATGAAACAGAAATGGTATTA 543
Qy      668  GCCAGCACCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 727
Db      544  GCCAGTACCAAGCGGCTAAAGCCATGGAGCAGATGGCAGGCTCGAGTGCAGGCGGCGGCGGCGG 603
Qy      728  GCCAUGGAGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 787
Db      604  GCCATGGAGGTGTCTAGTAAGGCTAGGCGAGTGTGTCAGGCAATGAGAACCAATTTGGGAGCC 663
Qy      788  CAGCCCGACAGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 847
Db      664  CACCCCTAGCTCAGTGGCGGTTTGAAGATGATCTCCTTGAAGATGATCTCCTTGAAGATGATCT 723
Qy      848  AAGCGCAUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 880
Db      724  AAACGGATGGGAGTGCAATGCAGCGATTCAAG 756
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Job time : 207.984 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-10-729-830-7
Perfect score: 1011
Sequence: 1 gcucgucucucuuucacagag.....aaaaaaaaaaaaaaaaa 1011

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

| Database : | Published Applications         | NA_Main:      |
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| 2:         | /cnm2_6/ptodata/1/pubpna/US08  | PUBCOMB.seq.* |
| 3:         | /cnm2_6/ptodata/1/pubpna/US09A | PUBCOMB.seq.* |
| 4:         | /cnm2_6/ptodata/1/pubpna/US09B | PUBCOMB.seq.* |
| 5:         | /cnm2_6/ptodata/1/pubpna/US10A | PUBCOMB.seq.* |
| 6:         | /cnm2_6/ptodata/1/pubpna/US10B | PUBCOMB.seq.* |
| 7:         | /cnm2_6/ptodata/1/pubpna/US10C | PUBCOMB.seq.* |
| 8:         | /cnm2_6/ptodata/1/pubpna/US10D | PUBCOMB.seq.* |
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| 10:        | /cnm2_6/ptodata/1/pubpna/US11  | PUBCOMB.seq.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query |        |   | DB               | ID                 | Description |
|------------|-------|-------|--------|---|------------------|--------------------|-------------|
|            |       | Match | Length |   |                  |                    |             |
| 1          | 1011  | 100.0 | 1011   | 8 | US-10-729-830-7  | Sequence 7, Appli  |             |
| 2          | 884   | 87.4  | 942    | 8 | US-10-729-830-6  | Sequence 6, Appli  |             |
| 3          | 842.4 | 83.3  | 844    | 8 | US-10-729-830-4  | Sequence 4, Appli  |             |
| 4          | 762   | 75.4  | 775    | 8 | US-10-729-830-3  | Sequence 3, Appli  |             |
| 5          | 608.8 | 60.2  | 942    | 8 | US-10-729-830-5  | Sequence 5, Appli  |             |
| 6          | 494   | 48.9  | 986    | 8 | US-10-866-484-9  | Sequence 9, Appli  |             |
| 7          | 485.8 | 48.1  | 774    | 8 | US-10-729-830-1  | Sequence 1, Appli  |             |
| 8          | 481.2 | 47.6  | 1027   | 6 | US-10-177-390-31 | Sequence 31, Appli |             |
| 9          | 479.6 | 47.4  | 1027   | 8 | US-10-855-875-5  | Sequence 5, Appli  |             |
| 10         | 477.6 | 47.2  | 1023   | 6 | US-10-065-133A-1 | Sequence 1, Appli  |             |
| 11         | 477.6 | 47.2  | 1023   | 7 | US-10-434-811A-1 | Sequence 1, Appli  |             |
| 12         | 477.6 | 47.2  | 1023   | 7 | US-10-734-373-1  | Sequence 1, Appli  |             |
| 13         | 477.6 | 47.2  | 1023   | 8 | US-10-872-014-1  | Sequence 1, Appli  |             |
| 14         | 477.4 | 47.2  | 816    | 6 | US-10-371-525-13 | Sequence 13, Appli |             |
| 15         | 477.4 | 47.2  | 816    | 6 | US-10-371-065-13 | Sequence 13, Appli |             |
| 16         | 477.4 | 47.2  | 816    | 6 | US-10-371-645-13 | Sequence 13, Appli |             |
| 17         | 477.4 | 47.2  | 816    | 6 | US-10-371-260-13 | Sequence 13, Appli |             |
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| 19         | 474.8 | 47.0  | 1023   | 7 | US-10-434-811A-4 | Sequence 4, Appli  |             |
| 20         | 474.8 | 47.0  | 1023   | 7 | US-10-734-373-4  | Sequence 4, Appli  |             |
| 21         | 474.8 | 47.0  | 1023   | 8 | US-10-872-014-4  | Sequence 4, Appli  |             |
| 22         | 474.2 | 46.9  | 756    | 6 | US-10-065-133A-3 | Sequence 3, Appli  |             |
| 23         | 474.2 | 46.9  | 756    | 7 | US-10-434-811A-3 | Sequence 3, Appli  |             |

## ALIGNMENTS

## RESULT 1

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US-10-729-830-7
; Sequence 7, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1011

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| Query Match           | 100.0%       | Score 1011;         | DB 8;      | Length 1011; |
|-----------------------|--------------|---------------------|------------|--------------|
| Best Local Similarity | 100.0%;      | Pred. NO. 3.1e-194; |            |              |
| Matches 1011;         | Conservative | 0;                  | Mismatches | 0;           |
|                       | Indels       | 0;                  | Gaps       | 0;           |

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|     |  |     |
| 1   | GCUGUUCUUUUUGCAGAGAAGCUCAGAAUAAACGCUAACTUUGGCAGAUUAAGAUGGC | 60  |
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| 61  | CGUACUGGCCCCCGCCGACCCUGGUGUGUGCGGCGCCUGGCGCCUGACCCAGAC     | 120 |
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| 61  | CGUACUGGCCCCCGCCGACCCUGGUGUGUGCGGCGCCUGGCGCCUGACCCAGAC     | 120 |
|     |  |     |
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| 121 | CUGGGGCAGCTUGCTUGACCGAGGUGAGACCUACUGTUGAGACUACUCCCCAGGGGCC | 180 |
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RESULT 2
US-10-729-830-6
; Sequence 6, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10729,830
; PRIORITY FILING DATE: 2003-12-05
; PRIORITY FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
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; SOFTWARE: PatentIn Ver. 2.1.1
; SEQ ID NO 6
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with increased G/C-content and
; OTHER INFORMATION: stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-6

Query Match      87.4%; Score 884; DB 8: Length 942;
Best Local Similarity 100.0%; Pred. No. 1.2e-168; Indels 0; Gaps 0;
Matches 884; Conservative 0; Mismatches 0;

QY 128 AGCCUCUGACACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCUGAAG 187
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Db 59 AGCCUCUGACACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAGCGGCCCCUGAAG 118
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QY 188 GCCGAGAUCCGCCAGAGGUGGAGGACGUGUUCGCCGCGCAAGAACACCGACCUAGGAGUG 247
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Db 119 GCCGAGAUCCGCCAGAGGUGGAGGACGUGUUCGCCGCGCAAGAACACCGACCUAGGAGUG 178
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QY 248 CUGAUGGAGUGGUGAAGACCGAGGCCCAUCCUGAGCCCCUUGACCAAGGCAUCCUGGGC 307
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Db 179 CUGAUGGAGUGGUGAAGACCGAGGCCCAUCCUGAGCCCCUUGACCAAGGCAUCCUGGGC 238
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QY 308 UUCGUGUUAUCCUCUGACCGUGCCAGCGAGCGCGGCGUGCAGCGCGCGCGUUCUGUGCAG 367
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Db 239 UUCGUGUUAUCCUCUGACCGUGCCAGCGAGCGCGGCGUGCAGCGCGCGCGUUCUGUGCAG 298
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|
|
QY 368 AACGCCCTUGAAACCGCAACCGCGGACCCCAACAUAUGGACCAAGGCGCGUGAAGCUGUA 427
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|
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Db 299 AACGCCCTUGAAACCGCAACCGCGGACCCCAACAUAUGGACCAAGGCGCGUGAAGCUGUA 358
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|
|
QY 428 AACGUAAGAGGAGGAGUAUCCUCCAGCGGCCCAAGAGAUACGCGUAGCUACAGCGCC 487
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|
|
Db 359 AACGUAAGAGGAGGAGUAUCCUCCAGCGGCCCAAGAGAUACGCGUAGCUACAGCGCC 418
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|
QY 488 GGGCGCCUUGCCAGCGUGCAUGGGCCUGAUUUAACAAGAGUAGGCGCGCGUGACCA 547
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|
|
Db 419 GGGCGCCUUGCCAGCGUGCAUGGGCCUGAUUUAACAAGAGUAGGCGCGCGUGACCA 478
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QY 548 GUGGCCUUCGGCCUGUGUGCGCCACUUGCGAGCAGAUUCGCCGACAGCCAGCCAGCCAGC 607
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|
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Db 479 GUGGCCUUCGGCCUGUGUGCGCCACUUGCGAGCAGAUUCGCCGACAGCCAGCCAGCCAGC 538
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QY 608 CACAGGAGAGUGGAGGACCAACCAACCCUUAUACAGGCGCAGAGAACAGAUUGGUGCUG 667
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Db 539 CACAGGAGAGUGGAGGACCAACCAACCCUUAUACAGGCGCAGAGAACAGAUUGGUGCUG 598
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QY 668 GCCAGACCAACCGCCAGGCGCAUGGAGCAGAUUGGCCGCGCAGCGAGCGAGCGCGCGAG 727
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Db 599 GCCAGACCAACCGCCAGGCGCAUGGAGCAGAUUGGCCGCGCAGCGAGCGAGCGCGCGAG 658
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QY 728 GCCAUGAGGUGGCCAGCGCAGGCGAGAUUGGUGCAGGCCAUGAGGACCAUUGCGGACC 787
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Db 659 GCCAUGAGGUGGCCAGCGCAGGCGAGAUUGGUGCAGGCCAUGAGGACCAUUGCGGACC 718
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QY 788 CACCCAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
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Db 719 CACCCAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 778
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QY 848 AAGCGCAUGGGCGUGCAGAGUAGCGCGCUUCAAAGUAACTUAGAGACUGACUAGCCCGCUGG 907
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Db 779 AAGCGCAUGGGCGUGCAGAGUAGCGCGCUUCAAAGUAACTUAGAGACUGACUAGCCCGCUGG 838
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; Publication No. US20050013826A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; APPLICANT: Shneider, A.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003CIP
; CURRENT APPLICATION NUMBER: US/10/866,484
; CURRENT FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 10/741,466
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-866-484-9

Query Match      48.9%; Score 494; DB 8; Length 986;
Best Local Similarity 66.5%; Pred. No. 5.1e-90;
Matches 504; Conservative 89; Mismatches 165; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGAGACCUACGUGUGAGCAUCAUCCCGAGCGGCCCGCUGAAG 187
Db 4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTATCGTCCGTCAGGCCCTCAA 63
Qy 188 GCCGAGAUCCGCGAGGUCGAGAGCGUGUUGCGCGCAAGAACACCGACUGAGGUG 247
Db 64 GCCGAGATCGCGCAGACTTGAAGATGTTCTTGTGGGAAGAACACCGCATCTCGAGCA 123
Qy 248 CUGAUGAGUGGUCGAGACGACGACGACCAUCCUGAGCCCGCUGACCAAGGGAUCCUGGC 307
Db 124 CTCATGGAATGGCTAAGCAAGAACCAATCTGTCACTCTGACTAAGGGGATTTAGGA 183
Qy 308 UUCGUGUACCCUGACCGUGCCGAGCGCGCGCCUGCAGCGCGCGCGCGCGCGCGCG 367
Db 184 TTTGTGTTACGCTCACCGTCCGAGTGAGCGAGGACTGCGAGCGTTGTCAG 243
Qy 368 AACGCCUUGAACGGCAACCGCGACCCCAACAAUAGCAAGGCGCGUGAAGCUGUACAG 427
Db 244 AATGCCCTTAATGGGAATGGGGATCCAAACCAATGAGACAGGCGAGTGAACCTGTACAG 303
Qy 428 AAGCUGAGAGGAGAGUACCUUCCAGCGCGCGCGAGGAGUACGCUUGAGCUACAGCGCC 487
Db 304 AAGCTCAAAAGGGGAATTAATTCACCGGGCCAAAGAAAGTAGCGCTCAGTTTACT 363
Qy 488 GCGCGCCUGCGCAGCUGCAUGGGCCUGAUCAACAGAGUAGGCGCGCGUGACCAACCGAG 547
Db 364 GTGCACTTGCAGCTGATGGGCTCATATACACAGATGGGGACTGTAACTTAACTGAA 423
Qy 548 GUGGCCUUGCGCUGUGUGCGCCACCGUGAGCAGAUCCGCGACAGCGACCGCAGC 607
Db 424 GTGGCATTTGGCTAGTGTGTGCCACTTTGTGAGCAGATTGTCGACTCCCGACATCGGTCC 483
Qy 608 CACAGGAGUAGUGUACACCAACCAACCCUUGAUCAGGACGACGAGAACAGAUUGUGUG 667
Db 484 CACAGACAGATGGTGACGACCAACCAACCCACTAATCAGACATGAGAACAGGATGGTGTG 543
Qy 668 GCCAGCACCGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 727
Db 544 GCCAGTACCGCTAAGGCCATGAGCAGATGGCAGGCTCGATGTGAACAGGAGGAGGAG 603
Qy 728 GCCAUGGAGGUGGCGAGCGAGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 787
Db 604 GCCATGGAGGTTGCTAGTCAGGCTAGGCGAGATGGTGCAGGCAATGAGAACCTTGGGACT 663
Qy 788 CACCCAGCAGGAGCGCGCGCUGAAGAACGACUUGCUGGAGAACUUGCAGGCGCUACAG 847
Db 664 CACCCTAGCTCCGCGCGGTCTAAAGATGATCTTCTTGAATAATTTGAGGCGCTTACAG 723
Qy 848 AAGCGCAUGGGGCGAGCAGUAGCAGCGCGCUCAAGUGAAC 885

; Publication No. US10729830-1
; GENERAL INFORMATION:
; APPLICANT: Pascolo, Steve
; APPLICANT: Hoerr, Ingmar
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Influenza virus
; FEATURE:
; OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
US-10-729-830-1

Query Match      48.1%; Score 485.8; DB 8; Length 774;
Best Local Similarity 65.4%; Pred. No. 2.2e-88;
Matches 498; Conservative 91; Mismatches 172; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGAGACCUACGUGUGAGCAUCAUCCCGAGCGGCCCGCUGAAG 187
Db 14 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTATCATCCGTCAGGCCCTCAA 73
Qy 188 GCCGAGAUCCGCGAGGUCGAGGAGCGUGUUGCGCGCAAGAACACCGACUGAGGUG 247
Db 74 GCCGAGATCGCAGAGACTTGAAGATGTTCTTGTGAGGGAAGAACACCGCATCTTGAAG 133
Qy 248 CUGAUGAGUGGUCGAGACGACGACGACCAUCCUGAGCCCGCUGACCAAGGGAUCCUGGC 307
Db 134 CTCATGGAATGGCTAAGCAAGAACCAATCTGTCACTCTGACTAAGGGGATTTAGGA 193
Qy 308 UUCGUGUACCCUGACCGUGCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db 194 TTTGTGTTACGCTCACCGTCCGAGTGAGGAGGACTGCGAGCGTAGACGCTTGTCCAA 253
Qy 368 AACGCCUUGAACCGCGAACCGCGACCCCAACAAUAGCAAGGCGCGUGAAGCUGUACAG 427
Db 254 AATGCCCTTAATGGGAACCGGGATCCAAATAACATGAGCAAGCAGTTAAACTGTATAGG 313
Qy 428 AAGCUGAGAGGAGAGUACCUUCCAGCGCGCGCAAGAGAGUACGCUUGAGCUACAGCGCC 487
Db 314 AAGCTCAAGAGGGAGATTAACATTTCCATGGGGCCAAAGANAATCTCACTCAGTTATTGCT 373
Qy 488 GCGCGCCUGCGCAGCUGCAUGGGCCUGAUCAACAGAGUAGGCGCGCGUGACCAACCGAG 547
Db 374 GTTGCACTTGCAGTTGTTATGGGCTCATATACACAGGATGGGGGTGTGACCACTGAA 433
Qy 548 GUGGCCUUGCGCUGUGUGCGCCACCGUGAGCAGAUCCGCGACAGCAACCGCAGCAGC 607
Db 434 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAAACAGATGCTGACTCCAGCATCGGTCT 493
Qy 608 CACAGGAGAGUAGGAGCACCAACCAACCCUUGAUCAGGACGACGAGAACAGAUUGUGUG 667
Db 494 CATAGGCAATGGTGTGCAACCAACCAACCCACTAATCAGATGAGAACAGAAATGGTTTA 553
Qy 668 GCCAGCACCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 727
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Db 554 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTCGATCGAGTGGACGAGCAGAG 613  
Qy 728 GCAUGAGAGUGGCGACGAGGCGAGGAGUGGUGGAGGCAUGAGGACCAUGCGCACC 787  
Db 614 GCCATGAGGTTGTAGTCAAGCTAGGCTAGGCAATGGTGCAGGGATGAGAACCATTTGGACT 673  
Qy 788 CACCCAGCAGCAGCGCGCCUGAAGAACGACACCUUGUGGAGAACCUUGCAGGCGCUACCG 847  
Db 674 CATCCTAGCTCCAGTGTGGTCTGAAATAATGATCTTCTTGAAATTTGCGAGGCTATCAG 733  
Qy 848 AAGCGCAUGGCGUGCAGUGCAGCGCGUUCNAGUGACUAG 888  
Db 734 AAACGAATGGGGTGCAGATGCAACGGTTCAAGTGAACCTAG 774

## RESULT 8

US-10-177-390-31  
; Sequence 31, Application US/10177390  
; Publication No. US20030143743A1  
; GENERAL INFORMATION:  
; APPLICANT: Schuler, Gerold  
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear  
; TITLE OF INVENTION: Polynucleotides by Electroporation  
; FILE REFERENCE: 021505wo/JH/ml  
; CURRENT APPLICATION NUMBER: US/10/177,390  
; CURRENT FILING DATE: 2002-06-20  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: Influenza virus  
US-10-177-390-31

Query Match 47.6%; Score 481.2; DB 6; Length 1027;  
Best Local Similarity 65.3%; Pred. No. 1.9e-87;  
Matches 495; Conservative 90; Mismatches 173; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGGAGACUACUGUGUGAGCAUCCCGAGCGGCCCCUGAAG 187  
Db 29 AGTCTTCTAACCGAGGTGGAACCTACGTTCTCTATCATCCCGTCAGGCCCCCTCAA 88  
Qy 188 GCCGAGAUCCGCCAGAGCGUGAGGA CGUGUUCGCCGCAAGAACACCGCAGGAGUG 247  
Db 89 GCCGAGATCGCACAGAGACTTGAAGATGCTTTGCGAGGAAGAACACCGATCTTGAAGTT 148  
Qy 248 CUGAUGAGUGGUGAAGACAGGCGCCAUCCUGAGCGCCUGACCAAGGGAUCCUGGGC 307  
Db 149 CTCATGGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAAGGGGATTTAGGA 208  
Qy 308 UUCGUGUACCCUGACCGUGCCAGCGAGCGCGCUGCAGCGCCGCGCUUGUGCAG 367  
Db 209 TTTGTGTTCAGCTCACCGTCCAGTAGGAGAGACTGCGAGCGTAGACGCTTTGTCCAA 268  
Qy 368 AACGCCUUGAAGCGGCAACCGCGACCCCAACAAUGGACAAAGGCGCGUGAAGCUGUACAGG 427  
Db 269 AATGCCCTTATGGNACGGGATCCAAATTAACATGGACAAGCAGTTAAACTGTATAGG 328  
Qy 428 AAGCUGAAGAGGGAGAUCAUCCUACACGCGCCCAAGGAGAUACGCGUGACUACAGCGCC 487  
Db 329 AAGCTCAAGAGGGAGATAAATTCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 388  
Qy 488 GGCGCCUGGCGACGUGCAGGCGCGUGAUCAACAGAGAGUGGCGCGUGACCAACCGAG 547  
Db 389 GGTGCATTTGCGCTGTATGGGCTCATATACAAAGATGGGGCTGTGACCACTGTAA 448  
Qy 548 GUGGCGCUUGGCGGUGGCGCCACCUUGCGAGCAGAUUGCGCGCAGCAGCAGCGCAGC 607  
Db 449 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCAGCATCGGTCT 508  
Qy 608 CACAGGCAUGAGUGGAGACCAACCAACCCUUGAUACAGGCGACGAGAACAGGAUGUGUG 667

Db 509 CATAGGCAAAATGTTGACAAACCAACCACTATCAGACATGAGAACAGATGGTTTAA 568  
Qy 668 GCCAGACCAACCGCCCAAGGCCAUGGAGCAGAUUGGCGGAGCAGCAGCAGGCGCGCAG 727  
Db 569 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCGAGTGCAGCAGCAGCAG 628  
Qy 728 GCAUGAGUGGCGCAGCAGCGCCAGGCGCAGAUUGGUGCAGGCCCAUGAGGAGCAUCGCA 787  
Db 629 GCCATGAGGTTGCTAGTCAGGCTAGGCAATGGTGCAGCGATGAGAACCATTTGGGACT 688  
Qy 788 CACCCAGCAGCAGCGCGCCUGAAGAACGACACCUUGUGGAGAACCUUGCAGGCGCUACCG 847  
Db 689 CATCCTAGCTCCAGTGTGGTCTGAAATAATGATCTTCTTGAAATTTGCGAGGCTATCAG 748  
Qy 848 AAGCGCAUGGCGUGCAGUGCAGCGCUUCAAUGAAG 885  
Db 749 AAACGAATGGGGTGCAGATGCAACGGTTCAAGTGATC 786

## RESULT 9

US-10-855-875-5  
; Sequence 5, Application US/10855875  
; Publication No. US20050003349A1  
; GENERAL INFORMATION:  
; APPLICANT: Kawaoka, Yoshihiro  
; TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene  
; FILE REFERENCE: 800.038US1  
; CURRENT APPLICATION NUMBER: US/10/855,875  
; CURRENT FILING DATE: 2004-05-27  
; PRIOR APPLICATION NUMBER: US 60/473,798  
; PRIOR FILING DATE: 2003-05-28  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: Influenza virus  
US-10-855-875-5

Query Match 47.4%; Score 479.6; DB 8; Length 1027;  
Best Local Similarity 64.6%; Pred. No. 4.1e-87;  
Matches 495; Conservative 92; Mismatches 179; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGGAGACUACUGUGUGAGCAUCCCGAGCGGCCCCUGAAG 187  
Db 29 AGTCTTCTAACCGAGGTGCAAAACGTACGTACTCTCTATCATCCCGTCAGGCCCCCTCAA 88  
Qy 188 GCCGAGAUCCGCCAGAGCGUGGAGGAGUGUUCGCCGCAAGAACACCGCAGGAGUG 247  
Db 89 GCCGAGATCGCACAGAGACTTGAAGATGCTTTTGCAGGGAAGAACACCGATCTTGAAGTT 148  
Qy 248 CUGAUGAGUGGUGAAGACAGCGCCCAUCCUGAGCGCCCGUGACCAAGGCAUCCUGGGC 307  
Db 149 CTCATGGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAAGGGGATTTAGGA 208  
Qy 308 UUCGUGUACCCUGACCGUGCCAGGAGCGCGCUGCAGCGCGCCCGCUGUGCAG 367  
Db 209 TTTGTGTTCAGCTCACCGTCCAGTAGGAGGAGACTGCGAGCGTAGACGCTTTGTCCAA 268  
Qy 368 AAGCCUUGAAGCGGCAACCGGACCCCAACAAUGGAGCAAGGCGCGUGAAGCUGUACAGG 427  
Db 269 AATGCCCTTAAATGGGAACCGGGATCCAAATTAACATGGACAAGCAGTTAACTGTATAGG 328  
Qy 428 AAGCUGAAGAGGGAGAUCAUCCUACCGCGCCCAAGGAGAUACGCGUGACUACAGCGCC 487  
Db 329 AAGCTCAAGAGGGAGATAAATTCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 388  
Qy 488 GGCGCCUGGCGCAGCUGCAGUGGCGCGUGAUCAACAGGAGUGGCGCGCGCAGCAGCAG 547  
Db 389 GGTGCATTTGCCAGTTGTATGGGCTCATATACAAAGATGGGGCTGTGACCACTGTAA 448  
Qy 548 GUGGCGCUUGGCGGUGGCGCCACCUUGCGAGCAGAUUGCGCGCAGCAGCAGCGCAGC 607

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Db 449 GTGGCATTTGGCTTGGTATGTGCAACCTGTGAAACAGATTGCTGACTCCCGACATCGGTCT 508
Qy 608 CACAGGAGAGUGGAGACACACCAACCCCGUGAUCAGGACGAGAACAGAGUUGUGUG 667
Db 509 CATAGGCAATGGTGACAAACCAATCCATTAATCAGATGAGAACAGAAATGGTTTA 568
Qy 668 GCCAGCACCAACCGCCAGGCGCAUGGAGCAGAGCCGCGAGCAGCGCGCGAG 727
Db 569 GCCAGCACTACAGCTAAGGCTATGGAGCAATGCTGGATCGATGAGCAAGCAGCAGAG 628
Qy 728 GCCAUGAGAGUGGCGACGCGCAGCAGGAGUGGAGGAGGAGGAGGAGGAGGAGGAGGAG 787
Db 629 GCCATGAGAGGTGTGCTAGGCTAGACAAATGCTGCAAGGATGAGAACCATTTGGGACT 688
Qy 788 CACCCAGCAGCAGCGCGCGCCGCAAGAACGACCCUGGAGAGACCCUGGAGGAGGAGGAGGAG 847
Db 689 CATCTAGCTCAGTGTGCTGAAATGATCTTCTTGAATTTTGCAGGCGCTATCAG 748
Qy 848 AAGCGCAUGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 893
Db 749 AAACGAATGGGGTGCAGATGCAACGGTTCAGGTGATCCTCTCACT 794
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## RESULT 10

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US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Publication No. US20030195074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1
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Query Match 47.2%; Score 477.6; DB 6; Length 1023;
Best Local Similarity 65.0%; Pred. No. 1e-86;
Matches 493; Conservative 90; Mismatches 175; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGGAGACCUACGUGUGAGGAGCAUCCCGAGCGGCCCGCCUGAAG 187
Db 28 AGTCTTCTGACCGAGGTGCAACGTAAGTCTCTATCTGATCATCAGGCCCGCCCTCAA 87
Qy 188 GCCGAGAUCCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 247
Db 88 GCCGAGATCGCGAGAGACTTGAAGATGTCTTTGACGGGAGGAGAACCGGATCTTGAGGCA 147
Qy 248 CUGAUGAGUGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 307
Db 148 CTCATGGAATGGCTAAAGAGCAAGACCAATCTGTCACTCTGATCAATGAAGGGATTTTGA 207
Qy 308 UUCGUGUACCCUGACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 367
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Db 208 TTGGTATTACGCTCACCGTCCCGAGTGCAGGAGGACTGCAGCGGTAGACGCTTTGTCCAA 267
Qy 368 AAGCCCGUAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 427
Db 268 AATGCCCTTATGTGGAACCGGAGATCCAAACAAATGGACAGAGCAGTAAACTGTACAGG 327
Qy 428 AAGCUGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 487
Db 328 AAGCTTAAAGAGAGAAATAACATTCATTCATGGGGGCAAGAGGTGGCACTTCAGCTATTCCACT 387
Qy 488 GGGCCCGUGGCGCAGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 547
Db 388 GGTGCACTAGCCAGCTGCATGGGACTCATATACACAGAAATGGGAACTGTGACAAACGAA 447
Qy 548 GUGGCCUUGCGGUGGUGGCGCACCCUGGAGCAGAGCCCGAGCAGCAGCAGCAGCAGCAGCAG 607
Db 448 GTGGCATTTTGGCCCTGTGTATGCGCCACATGTGAACAGATCGCTGATTTCCAGCATCTGATCT 507
Qy 608 CACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 667
Db 508 CACAGGAGATGTGAGCAACAAACCAACCCATTAAATCAGACATGAAACAGAAATGTTATTA 567
Qy 668 GCCAGCACCAACCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 727
Db 568 GCCAGTACCAACGCTAAAGCCATGGAGCAGATGGCAGGCTCGAGTGCAGGAGGAGGAGGAG 627
Qy 728 GCCAUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 787
Db 628 GCCATGAGGTTTGTAGTAAGGCTAGGCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 687
Qy 788 CACCCAGCAGCAGCGCGCGCCUGAAGACGACGUGGAGGAGGAGGAGGAGGAGGAGGAGGAG 847
Db 688 CACCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTTGAATTTTGCAGGCGCTACAG 747
Qy 848 AAGCGCAUGGCGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 885
Db 748 AAACGGATGGGAGTGCAAAATGCAGCGATTCAAGTGATC 785
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## RESULT 11

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US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CL-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1
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Query Match 47.2%; Score 477.6; DB 7; Length 1023;
Best Local Similarity 65.0%; Pred. No. 1e-86;
Matches 493; Conservative 90; Mismatches 175; Indels 0; Gaps 0;

QY 128 AGCUCUGACCGAGGUGGAGACUAGUGUGGAGCAUCCAGCGGCCGCCUUGAG 187
DB 28 AGTCTTCTGACCGAGGTGGAACGTAAGTCTCTCTATCTGATCATCAGGCCCTCAAA 87

QY 188 GCCGAGAUCCCGAGGUGGAGGACUGUUGCCGCGCAAGAACACCGACCGUGAGG 247
DB 88 GCCGAGATCGCGAGAGACTTGAAGTGTCTTTGCGAGGAGAACACCGATCTTGAGGCA 147

QY 248 CUGAUGAGUGGUGAAGACAGCGCCCAUCUCUGAGGCCUUGACCAAGGCGUCCUGGCC 307
DB 148 CTCATGGAATGGCTAAGACAGACCAATCTGTACCTCTGACTTAAGGGATTTAGGA 207

QY 308 UUCGUGUACACCGUACCGGCCAGCGCGCCUUGAGCAUCCAGCGGCCCGUUGGCG 367
DB 208 TTGCTATTACCGCTCACCGTCCAGTGAGCGAGGACTGCGAGCGTAGACGCTTGTCCAA 267

QY 368 AACGCCUGAACCGCGAGGAGGACCCCAACAAUGGACAGGCGGUGAAGCUGUACAGG 427
DB 268 AATGCCCTTAGTGGAACCGAGATCCAAACAAATGGAAGTGGAACTGTGACAAACGAA 447

QY 428 AAGCUGAAGGAGGAGUACUCCUCCAGCGCGCCAGAGCAUCCAGCGGCCCGCGCG 487
DB 328 AAGCTTAAAGAGAAATATCATTTCCATGGGCAAGAGAGGTGCGACTTCAGTATTCAC 507

QY 508 CACAGGAGUGGUGACCAACCAACCCUUGAUCAGGACGAGCAUCCAGCGGCCCGCG 567
DB 568 GCCAGTACCGGCTAAGCCATGGAGCAGATGGCAGGGTCCGAGTGAGCAGGCGAGAG 627

QY 608 GCGCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
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QY 848 AAGCGAUGGGGUGGAGUAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 885
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## RESULT 12

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US-10-734-373-1
; Sequence 1, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
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; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, x = a or g
; OTHER INFORMATION: At amino acid residue 213, xaa = val
; US-10-734-373-1
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Query Match 47.2%; Score 477.6; DB 7; Length 1023;
Best Local Similarity 65.0%; Pred. No. 1e-86;
Matches 493; Conservative 90; Mismatches 175; Indels 0; Gaps 0;

QY 128 AGCUCUGACCGAGGUGGAGACUACUGUGGAGCAUCCAGCGGCCGCCUUGAG 187
DB 28 AGTCTTCTGACCGAGGTGGAACGTAAGTCTCTCTATCTGATCATCAGGCCCTCAAA 87

QY 188 GCCGAGAUCCCGAGGUGGAGGACUGUUGCCGCGCAAGAACACCGACCGUGAGG 247
DB 88 GCCGAGATCGCGAGAGACTTGAAGTGTCTTTGCGAGGAGAACACCGATCTTGAGGCA 147

QY 248 CUGAUGAGUGGUGAAGACAGCGGCCCAUCUCUGAGGCCUUGACCAAGGCGUCCUGGCC 307
DB 148 CTCATGGAATGGCTAAGACAGACCAATCTGTACCTCTGACTTAAGGGATTTAGGA 207

QY 308 UUCGUGUACACCGUACCGGCCAGCGCGCCUUGAGCAUCCAGCGGCCCGUUGGCG 367
DB 208 TTGCTATTACCGCTCACCGTCCAGTGAGCGAGGACTGCGAGCGTAGACGCTTGTCCAA 267

QY 368 AACGCCUGAACCGCGAGGAGGACCCCAACAAUGGACAGGCGGUGAAGCUGUACAGG 427
DB 268 AATGCCCTTAGTGGAACCGAGATCCAAACAAATGGAAGTGGAACTGTGACAAACGAA 327

QY 428 AAGCUGAAGGAGGAGUACUCCUCCAGCGCGCCAGAGCAUCCAGCGGCCCGCGCG 487
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QY 488 GCGCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 547
DB 388 GGTGCACTAGCGAGCTGCGACTCATATACACAGAAATGGGAACTGTGACAAACGAA 447

QY 548 GUGGCCUUGGCCUUGGUGCGCCAGCGAGCAUCCAGCGGCCCGAGCGAGCGCGCGCG 607
DB 448 GTGGCATTTGGCTTAAAGCCATGGAGCAGATGGCAGGGTCCGAGTGAGCAGGCGAGAG 627

QY 608 GCGCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
DB 448 GTGGCATTTGGCTTAAAGCCATGGAGCAGATGGCAGGGTCCGAGTGAGCAGGCGAGAG 507

QY 608 CACAGCAGUUGGUGACCAACCAACCCUUGAUCAGGACGAGCAUCCAGCGGCCCGCG 667
DB 508 CACAGGAGATGAGTGAACCAACCAACCCATTAATCAGATGSTRCAGGCATGAGAACCATTTGGGACC 567

QY 668 GCCAGTACCGGCTAAGCCATGGAGCAGATGGCAGGGTCCGAGTGAGCAGGCGAGAG 727
DB 568 GCCAGTACCGGCTAAGCCATGGAGCAGATGGCAGGGTCCGAGTGAGCAGGCGAGAG 627

QY 728 GCGCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 787
DB 628 GCCATGAGGTTGCTAGTAGGCTAGCGAGATGSTRCAGGCATGAGAACCATTTGGGACC 687

QY 788 CACCCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
DB 688 CACCTAGCTCCAGTCCGCGTTTGAAGATGATCTCCTTGAATAATTTGCGAGGCTAC 747

QY 848 AAGCGAUGGGGUGGAGUAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 885
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Db 154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGCAACCAATCTTG 213
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Db 214 TCACCTCTGACTAAGGGAATTTAGGGTTTGTGTTCACTCGCTCAAGCGTGGCCAGTGGAGCA 273
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Db 274 GGAATGCGAGGTAGACGATTTGTCCTAAATGCCCCCTAAATGGGAATGGAGACCCCAAC 333
Qy 401 AUGACAAAGCGCCUGAAGUAGUACAGGAAGCUGAAGAGGAGAGAUCAUCCUCCACGGCGCC 460
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Qy 461 AAGGAGAUACGAGCUACAGCGCGCGCCUGGCGCCUGGCGUAGUGGCGCUAGAUCAUC 520
Db 394 AAGGAAGTTGCACTCACTTACTCAACTGGTGGCTTGGCCAGTTGCATGGGTCTCATATAC 453
Qy 521 AACAGGAGGCGCGUGACCAAGCGAGGUGGCGCUUGGCGCGUGGUGGCGCCACCGGAG 580
Db 454 AACCGGATGGGAACAGTGAACAGAAAGTGGCTCTTGGCCCTAGTATGTGCACTTTGTAG 513
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Qy 701 GCGGCGAGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 760
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Qy 761 GUGCAGGCGCAUGAGGAGCAUCCGCGCACCCAGCGAGCGCGCGCGCGCGCGCGCGCGCG 820
Db 694 GTGCGAGCAATGAGGAGCAATTTGGGACTCAACCTAGCTCCAGTGCAGTCTTAAAGATGAT 753
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Qy 881 UGA 883
Db 814 TGA 816
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US-10-371-069-13
; Sequence 13, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 816
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
; OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
; OTHER INFORMATION: influenza matrix protein gene
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)...(816)
; OTHER INFORMATION: PADRE-Influenza matrix
; US-10-371-069-13
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Best Local Similarity 64.4%; Pred. No. 1.1e-86;
Matches 504; Conservative 88; Mismatches 191; Indels 0; Gaps 0;
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Db 94 TCTATCATCCATCAGCGCGCCCGCTCAAAGCGCGAGATCGCGCAGAGACTTGAGGATGTTT 153
Qy 221 GCGGCAAGAAACACCGACCCUGGAGGUGUGAUGGAGUGGCGUGAAGAGACACGAGGCGCAUCCUG 280
Db 154 GCAGGGAAGAAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAGACCAATCTCTG 213
Qy 281 AGCCCCCUGACCAAGGCGCAUCCUGGCGUUGGCGUUCACCCUGACCGUGGCCAGCGAGCGC 340
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Db 274 GGAAGTCAAGTGAAGGAGTCTTGTCCAAATTTGCTTAAATGGGAAATGGAGACCCCAAC 333
Qy 401 AUGGCAAGCGCGUGAAGCUGUACAGGAAGCUGAAGGAGGAGAUCAUCCUCCACGCGCGC 460
Db 334 ATGGAAGGCGCGATTTAACTATACAGAGAGCTGAAGAGGGAATGACATTTCCATGGAGCA 393
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Db 394 AAGGAATGTCAGTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 453
Qy 521 AACAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 580
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Qy 641 AUCAGGCAAGAGAAACAGGAUUGGUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 700
Db 574 ATCAGGCAATGAGAAACAGAAATGGTACTAGCCAGCACTACGGCTAAGGCGCATGGAGCAATG 633
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Qy 881 UGA 883
Db 814 TGA 816
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
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Perfect score: 1011  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues  
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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 730.6 | 72.3        | 756    | 12    | US-11-131-479-27   |
| 2          | 686.8 | 67.9        | 759    | 12    | US-11-131-479-27   |
| 3          | 686.8 | 67.9        | 1050   | 12    | US-11-131-479-59   |
| 4          | 665.4 | 65.8        | 982    | 12    | US-11-131-479-61   |
| 5          | 664.8 | 65.8        | 759    | 12    | US-11-131-479-79   |
| 6          | 594.6 | 58.8        | 756    | 12    | US-11-131-479-26   |
| 7          | 488   | 48.3        | 756    | 12    | US-11-131-479-3    |
| 8          | 476.4 | 47.1        | 1027   | 12    | US-11-131-479-3    |
| 9          | 473   | 46.8        | 1305   | 12    | US-11-131-479-45   |
| 10         | 460.4 | 45.5        | 987    | 12    | US-11-155-478A-131 |
| 11         | 454   | 44.9        | 982    | 12    | US-11-131-479-60   |
| 12         | 454   | 44.9        | 4822   | 12    | US-11-131-479-95   |
| 13         | 454   | 44.9        | 5161   | 12    | US-11-131-479-101  |
| 14         | 454   | 44.9        | 5398   | 12    | US-11-131-479-91   |
| 15         | 454   | 44.9        | 7798   | 12    | US-11-131-479-97   |
| 16         | 454   | 44.9        | 7798   | 12    | US-11-131-479-98   |
| 17         | 454   | 44.9        | 7798   | 12    | US-11-131-479-99   |
| 18         | 454   | 44.9        | 7798   | 12    | US-11-131-479-100  |
| 19         | 454   | 44.9        | 8442   | 12    | US-11-131-479-106  |
| 20         | 454   | 44.9        | 8442   | 12    | US-11-131-479-107  |

|    |       |      |      |    |                     |                   |
|----|-------|------|------|----|---------------------|-------------------|
| 21 | 454   | 44.9 | 8450 | 12 | US-11-131-479-104   | Sequence 104, App |
| 22 | 454   | 44.9 | 8450 | 12 | US-11-131-479-105   | Sequence 105, App |
| 23 | 447.6 | 44.3 | 1027 | 12 | US-11-155-478A-130  | Sequence 130, App |
| 24 | 401.8 | 39.7 | 629  | 9  | US-11-137-807-18    | Sequence 18, Appl |
| 25 | 77.4  | 7.7  | 1180 | 12 | US-11-116-746-2     | Sequence 2, Appl1 |
| 26 | 77.4  | 7.7  | 1180 | 12 | US-11-116-746-4     | Sequence 4, Appl1 |
| 27 | 75.8  | 7.5  | 588  | 12 | US-11-136-527-1488  | Sequence 1488, Ap |
| 28 | 75.8  | 7.5  | 588  | 12 | US-11-136-527-5584  | Sequence 5584, Ap |
| 29 | 75.4  | 7.5  | 1677 | 7  | US-10-515-547-3     | Sequence 3, Appl1 |
| 30 | 75.2  | 7.4  | 4339 | 8  | US-10-909-125-801   | Sequence 801, App |
| 31 | 74.8  | 7.4  | 2475 | 9  | US-11-197-133A-17   | Sequence 17, Appl |
| 32 | 74.8  | 7.4  | 5152 | 8  | US-10-240-708-47    | Sequence 47, Appl |
| 33 | 74.6  | 7.4  | 1395 | 8  | US-10-955-054A-111  | Sequence 111, App |
| 34 | 74.6  | 7.4  | 2217 | 7  | US-10-947-249-197   | Sequence 197, App |
| 35 | 74.6  | 7.4  | 3819 | 7  | US-10-973-115B-405  | Sequence 405, App |
| 36 | 74.6  | 7.4  | 3819 | 8  | US-10-131-826A-405  | Sequence 405, App |
| 37 | 74.4  | 7.4  | 600  | 12 | US-11-136-527-6371  | Sequence 6371, Ap |
| 38 | 74.4  | 7.4  | 2020 | 12 | US-11-090-617-697   | Sequence 697, App |
| 39 | 74.4  | 7.4  | 2430 | 7  | US-10-649-457-3     | Sequence 3, Appl1 |
| 40 | 74.4  | 7.4  | 3015 | 12 | US-11-183-136-39    | Sequence 39, Appl |
| 41 | 74.4  | 7.4  | 4409 | 12 | US-11-136-527-2275  | Sequence 2275, Ap |
| 42 | 74.2  | 7.3  | 1905 | 8  | US-10-947-249-132   | Sequence 132, App |
| 43 | 74    | 7.3  | 1690 | 12 | US-11-090-439-43    | Sequence 43, Appl |
| 44 | 73.8  | 7.3  | 588  | 8  | US-10-689-742-41    | Sequence 41, Appl |
| 45 | 73.6  | 7.3  | 762  | 9  | US-11-096-568A-1243 | Sequence 1243, A  |

ALIGNMENTS

RESULT 1  
US-11-131-479-27  
; Sequence 27, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131.479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 27  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein  
US-11-131-479-27

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| Matches               | 650   | Conservative  | 89      | Mismatches | 14 | Indels | 0   |
| Gaps                  | 0     |   |         |            |    |        |     |
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; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for the M2M1 Fusion from VR4755
US-11-131-479-59

Query Match      67.9%; Score 686.8; DB 12; Length 1050;
Best Local Similarity 82.6%; Pred. No. 4.1e-72;
Matches 623; Conservative 89; Mismatches 42; Indels 0; Gaps 0;

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Db 297 CTTGCTGACAGAAAGTGAACAATACGCTGAGCATCGTGCACGCGGCCCCCTGAAGGC 356

QY 190 CGAGAACCCAGAGCGGUGGAGGAGCGUGUCCGCCCAAGAACACCGACCUUGGAGGUCU 249
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QY 250 GAUGGAGUGGUGAAGACACGAGCCCAUCCUGAGGCCCCUGACCAAGGGCAUCCUGGGCUU 309
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QY 550 GGCCUUCGCGGCGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 609
Db 717 GGCCTTCGCTGTGTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 776

QY 610 CAGGCGAGUUGGAGCCACCAACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 669
Db 777 CAGACAGATGTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 836

QY 670 CAGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 729
Db 837 CAGCACCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 896

QY 730 CAUGGAGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 789
Db 897 CATGGAGATCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 956

QY 790 CCCGAGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 849
Db 957 CCCGAGCAGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1016

QY 850 GCGCAUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 883
Db 1017 GAGAAATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1050
```

RESULT 4

```
US-11-131-479-61
; Sequence 61, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
```

```
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Codon Optimized Segment 7 from VR4763
US-11-131-479-61
```

```
Query Match      65.8%; Score 665.4; DB 12; Length 982;
Best Local Similarity 80.2%; Pred. No. 1.3e-69;
Matches 612; Conservative 90; Mismatches 61; Indels 0; Gaps 0;

QY 128 AGCCUGCUGACCGGAGGAGACCUACGUCUGAGCAUCAUCCACGCGGCCCCCUAGAG 187
Db 4 AGCCTGCTGACCGAGGTGGAACGATGTTCTCTATCTGCTGCGCGCGGCCCTGAAG 63

QY 188 GCCGAGAUCCGCCAGGCGUGGAGGAGCGUGUCCGCCCAAGAACACCCGACCUAGGUG 247
Db 64 GCCGAGATCGCCAGAGACTGGAGGAGCTGTTGCCCGGCAAGAACACCGACTGGAGGCC 123

QY 248 CUGAUGGAGUGGUGAAGACAGGCCCAUCCUGAGCCCCUGACCAAGGGCAUCCUGGGC 307
Db 124 CTGATGAGTGGCTGAAGACAGACAGACCCTCTGAGCCCCCTGACCAAGGGCATCTGGGC 183

QY 308 UUCGUGUACCCUGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367
Db 184 TTGCTGTTCACCTGACCGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 243

QY 368 AACGCCUUGAACGCGCAACGCGCGCCCAACAAUGAGCAAGGCGCGGUGAGCUUACAGG 427
Db 244 AACGCCCTGAACGCGCAACGCGGCGCCCAACAACTGACAGAGCGGTGAAGCTGTACAGA 303

QY 428 AAGCUGAAGAGGAGAUACACUCCACGCGGCCCAAGAGAUACUCCUGAGCUACAGCGCC 487
Db 304 AAGCTGAAGAGAGAGATCACTTCCACGCGCGCAAGGAGATCGCCCTGAGCTACAGCGCC 363

QY 488 GGCGCCUUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 547
Db 364 GGCGCCCTGGCCAGCTGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 423

QY 548 GUGGCCUUCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 607
Db 424 GTGGCCCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 483

QY 608 CACAGGCGAGUUGAGUACACACCAACCCUUGAUCAGGCGACGAGAACAGAGUUGUGUG 667
Db 484 CACAGACAGATGTGTGGCCACCAACCCCTCTGATCAGACACGAGAACAGAAATGCTGCTG 543

QY 668 GCGACACACCGCGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 727
Db 544 GCCAGCACCAACCGCGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 603

QY 728 GCCAUGGAGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 787
Db 604 GCCATGGAGATCGCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 663

QY 788 CACCCGAGCAGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 847
Db 664 CACCCGAGCAGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 723

QY 848 AAGCGCAUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 890
Db 724 AAACGAATGGGGGTGAGATGCAACGATTCAAGTAGTACCCCGCTG 766
```

```
RESULT 5
US-11-131-479-79
; Sequence 79, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 79
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Optimized M1 Coding Region
US-11-131-479-79

Query Match      65.8%; Score 664.8; DB 12; Length 759;
Best Local Similarity 80.7%; Pred. No. 1.6e-69;
Matches 610; Conservative 89; Mismatches 57; Indels 0; Gaps 0;

Qy      128 AGCCUGUGACCGGAGGAGACCUACGUGUGAGCAUCCGCCAGCGGCCCCCUAGAAG 187
Db      4 AGCTGTGACCGAGGTGCGAAGCTATGTTCTCTATGTCGCCAGCGGCCCTGAAG 63

Qy      188 GCCGAGAUCCGACAGCGGAGGAGACGUGUUGCGCGGCAAGAACACCGACCUAGGUG 247
Db      64 GCCGAGATCGCCAGACTGGAGGACGTGTTTCGCCGCGCAAGAACACCGACCTGGAGCC 123

Qy      248 CUGAUGGAGUGGUGGAGACCGCCCAUCCUGAGCCGCCUGACCAAGGGAUCCUGGGC 307
Db      124 CTGATGGAGTGGCTGAAGACAGACCCATCTCTGAGCCCTTGACACAGGGGATCTGTGGC 183

Qy      308 UUCGUGUUCACCCUGACCGGCGCCAGGAGCGCGCCUGAGCGCGCGCGUUCUGAG 367
Db      184 TTCGTGTTACCTTGACCGTGCCCGAGCGAGAGGCGCTGCAGAGAAGATTCGTGCAG 243

Qy      368 AACGCCUGAAGCGGAGUACACCUCCACGCGCGCAAGGAGAUCCUGAGCUACAGCGCC 427
Db      244 AACGCCCTGAACGGCAACCGGCGCCCAACCAACATGGAACAGACCGTGAAGCTGTACAGA 303

Qy      428 AAGCUGAAGAGGAGUACCUUCCACGCGCGCAAGGAGUACAGCGCGCUAGAGCUACAGCGCC 487
Db      304 AAGCTGAAGAGAGATCACCTTTCACGCGCGCAAGGAGATGCGCCTGAGCTACAGCGCC 363

Qy      488 GCGCGCCUGGCGCAGUGCAUGGCGCGUACUACAAAGGAGGCGCGCGUACCAACCGAG 547
Db      364 GCGCGCTTGGCGCTGATGGCGCTGTACACAGATGCGCGAGCGCGCGTCAACACCGAG 423

Qy      548 GUGGCUUUGGCGUGGUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
Db      424 GTGGCTTTCGCGCTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 483

Qy      608 CACAGGAGAGUGGUGGAGUACCAACCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
Db      484 CACAGAGAGATGTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 543

Qy      668 GCCAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
Db      544 GCCAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 603

Qy      728 GCCAUGGAGGUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 787
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Db      604 GCCTGTGAGATGCCAGCGCCAGCCAGACAGATGGTGCCAGGCATGAGCCATCGGCACC 663

Qy      788 CACCCCGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db      664 CACCCCGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 723

Qy      848 AAGCGCAUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 883
Db      724 AACGAATGGGGGTGCAGATGCAACGATTCAAGTGA 759

RESULT 6
US-11-131-479-28
; Sequence 28, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 28
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-28

Query Match      58.8%; Score 594.6; DB 12; Length 756;
Best Local Similarity 75.0%; Pred. No. 2.2e-61;
Matches 565; Conservative 89; Mismatches 99; Indels 0; Gaps 0;

Qy      128 AGCCUGUGACCGGAGGAGACCUACGUGUGAGCAUCCGCCAGCGGCCCCCUAGAAG 187
Db      4 AGTCTGTGACAGAGGTGAGACGTGCTGTCTCATCATTCCTCAGCGGCCCTGAAG 63

Qy      188 GCCGAGAUCCGCCAGAGCGGAGGAGCGUGUUGCGCGCAAGAACACCGACCUAGGUG 247
Db      64 GCCGAGATTGCCAGAGACTGGAGGAGCTCTTCGCCGCGCAAGAACACCGATCTGGAGGTG 123

Qy      248 CUGAUGGAGUGGUGGAGACCGCCCAUCCUGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
Db      124 CTGATGGAGTGGCTGAAGACTCGCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 183

Qy      308 UUCGUGUUCACCCUGACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db      184 TTCGTATTATCACTGACCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 243

Qy      368 AACGCCUGAAGCGGAGUACCUUCCACGCGCGCAAGGAGUACAGCGCGCUAGAGCUACAGCG 427
Db      244 AACGCCCTGAACGGCAACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 303

Qy      428 AAGCUGAAGAGGAGUACCUUCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
Db      304 AAGCTGAAGAGAGATCACATTTTCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 363

Qy      488 GCGCGCCUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 547
Db      364 GCGCGCTTGGCGCTGTGATGAGAGATGAGTATACAAAGATGGCGCGCGCGCGCGCGCGCG 423

Qy      548 GUGGCUUUGGCGUGGUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
```

Db 424 GTAGCCCTTTGGCTGTCTGCGCCACTTGCAGCAGATCGCGACTCTCAGCATAGATCT 483  
QY 608 CACAGCAGUUGUGACCAACCAACCCUUGAUCAGGCACGAGAACAGGAGUGUGUG 667  
Db 484 CACAGACAGATGGTGAAGACTACAAACCCCTGTATAGCGCAGAGAACAGGATGGCTG 543  
QY 668 GCCAGACACCGCCCAAGGCCAUGGAGCAGUUGGCCGCGCAGCAGGAGCAGCCGCCGAG 727  
Db 544 GCCTCTACTACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGTGGCAGCGCCGCCGAG 603  
QY 728 GCCAUGGAGUGGCCAGCCAGCCAGCGCAGAGUUGUGCAGGCCAUGAGGACCAUCGCCACC 787  
Db 604 GCATGGAGGTAGCTTCACAGGCCAGCGCAGATGGTGCAGGCCATCGCAACCATCGCACT 663  
QY 788 CACCCAGCAGCAGCCCGCCGCGUGAAGAACGACCCUGCUGGAGAACCCUGCAGGCCCUACAG 847  
Db 664 CACCCCTCAGCTCTGCGCGCTGAAGAACGACCTGCTGGAGAACCTGAGGCCCTATCAG 723  
QY 848 AAGCGCAUGGCGUGCAGUAGCAGCGCCUUAAG 880  
Db 724 AAGAGAAATGGCGCTACAGATGCAGAGGTTCAAG 756

## RESULT 7

US-11-131-479-26  
; Sequence 26, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 26  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein  
US-11-131-479-26

Query Match 48.3%; Score 488; DB 12; Length 756;  
Best Local Similarity 66.2%; Pred. No. 5.5e-49;  
Matches 498; Conservative 89; Mismatches 165; Indels 0; Gaps 0;  
QY 128 AGCCUGUACCGCAGGUGAGACCUAGCUGUGAGCAUCAUCCCGCGGCCGCCUGAAG 187  
Db 4 AGCTTGCTAAACAGAGTGAACCTATGTCCTCAGTATCTTCTAGCGGCCCTTAAA 63  
QY 188 GCCGAGUCCGCCAGGCGUGAGCAGUUGUCCGCGGCAAGAACACCGACUGAGGUG 247  
Db 64 GCCGAAATCGCTCAGCGGCTCGAGGATGTTTTGCGCGCAAGAACACCGACCTGAGGTA 123  
QY 248 CUGAUGGAGUGGTCUAGAACACGAGCCCAUCCUGAGCCCGCCUGACCAAGGCAUCCUGGCG 307  
Db 124 TTGATGGAGTGGCTGAACACGACCTATCTTGAGGCCCTCTACTAAGGGAACTACTCGG 183  
QY 308 UUCGUGUACCCUCCAGCCGUGCCCGCAGCGCGCGCUGCAGCGCGCGCGUUCUGGAG 367  
Db 184 TTGCTTTTACATTGACCGTGCCTCAGAGAGGGGTCTCCAAAGAGGGCGCTTCGTGAG 243  
QY 368 AACGCCUUGAACGCCCAACCGCGACCCCAACAAUUGGACAAAGCCCGUGAAGCUGUACAG 427  
Db 244 AACGCCTTAAACGGGAAACGGGACCCCAATAATATGGATAGGCACTGAACTGTATCGC 303

QY 428 AAGCUGAAGAGGAGAUCAUCCUCCACGCGCCAAAGAGAUCAUCCUGAGCUACAGCGCC 487  
Db 304 AAATTAAAGCGGAGATAACCTTCCATGGAGCCAGGAGATCTCCCTGTCTTACTCTGCA 363  
QY 488 GCGCGCCUGGCGCAGCUGAGUGGCCUGAUCUUAACAGAUUGGGCGCCUGUACCAACCGAG 547  
Db 364 GGTGCTCTCGGCTCGTGTATGGGACTTATCTACAAACCAATGGGCGCGCTCAACAGAA 423  
QY 548 GUGGCUUUGCGCUGUGUGCGCCACUGCGGAGCAGAUCCGCGCAGCAGCAGCAGCCGAGC 607  
Db 424 GTGGCTTTTGGGCTGTGTGCGCAACTTTCGCAACAGATTGCTGACAGTCAGCAGCCGCTCC 483  
QY 608 CACAGCAGUUGUGAGCACCACCAACCCUUGAUCAGGCACGACAGAACAGGAGUGUGUG 667  
Db 484 CACCGTCAAAATGGTCACCAACCAACCATCGCTGATTAGCATGAAATTCGATGTTCTA 543  
QY 668 GCCAGCACACCGCCCAAGGCCAUGGAGCAGUAGUGGCCGCGCAGCAGCGCGCCCGAG 727  
Db 544 GCATCAACTACAGCCAAAGCAATGGAAACAATGGCGCGAAGCTCCGAGCAGGCTGCCGAG 603  
QY 728 GCCAUGGAGUGGCCAGCCAGCGCGCGUGAAGAACGACCCUGCUGGAGAACCUAGAGCAACCGCACC 787  
Db 604 GCGATGGAGGTGGCGTCCAGGCCACAGACAGATGGTACAGGCTATGAGAACTATCGGTACG 663  
QY 788 CACCCAGCAGCAGCGCGCGCGUGAAGAACGACCCUGCUGGAGAACCUAGCGGCCUACAG 847  
Db 664 CACCCAGTCTTTCAGCTGGGCTGAAGAAATGATCTTCTTGAGAACCTCGAGGCCCTACCNA 723  
QY 848 AAGCGCAUGGCGUGCAGUAGCAGCGCCUUA 879  
Db 724 AAGCGATGGCGTCCAGATGCAGAGATTAA 755

## RESULT 8

US-11-131-479-3  
; Sequence 3, Application US/11131479  
; Publication No. US20060024670A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, Catherine J.  
; APPLICANT: Vilalta, Adrian  
; APPLICANT: Wloch, Mary K.  
; APPLICANT: Evans, Thomas G.  
; APPLICANT: Geall, Andrew J.  
; APPLICANT: Jimenez, Gretchen  
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use  
; FILE REFERENCE: 1530.0640002/EJH/J-H  
; CURRENT APPLICATION NUMBER: US/11/131,479  
; CURRENT FILING DATE: 2005-05-18  
; PRIOR APPLICATION NUMBER: US 60/571,854  
; PRIOR FILING DATE: 2004-05-18  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 3  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: Influenza A virus  
US-11-131-479-3

Query Match 47.1%; Score 476.4; DB 12; Length 1027;  
Best Local Similarity 64.9%; Pred. No. 1.2e-47;  
Matches 492; Conservative 90; Mismatches 176; Indels 0; Gaps 0;  
QY 128 AGCCUGUACCGCAGGUGAGACCUAGCUGUGAGCAUCAUCCCGCGGCCGCCUGAAG 187  
Db 29 AGTCTTCTAACCGAGGTGGAACCGTACGTACTCTCTATCATCCCGCTCAGGCCCTCAAA 88  
QY 188 GCCGAGUCCGCCAGGCGAGCAGUUGUCCGCGGCAAGAACACCGACUGAGGUG 247  
Db 89 GCCGAGATCGCAGAGACCTTGAAGATGCTTTGAGGGGAAGAACACTGATCTTGAGGTT 148  
QY 248 CUGAUGGAGUGGCGUAGAGACCGAGGCCCAUCCUGAGCCCGCCUGACCAAGGCAUCCUGGCG 307

|    |  |     |  |     |
|----|--|-----|--|-----|
| Dd |  | 149 | CTCATGGAATGGCTAAAGACAAAGCCAAATCCTGTGCACCTCTGTAGACTAAGGGGATTTTTAGGA | 208 |
| Qy |  | 308 | UUCUGGUUACCCUGAACCGUGCCCAGCGCGGCCCUUCAGCGCCGCGUUCUGUGCAG           | 367 |
| Dd |  | 209 | TTTGTGTTTCACGCTCACCGTGCCAGTGAGCGAGGACTGCGAGCGTAGACGCTTTGTCCAA      | 268 |
| Qy |  | 368 | AACGCCCTGAAACGGCAACGGCGACCCCCAAACAUAUGGACAAGGCCGUGAAGUGUAACAGG     | 427 |
| Dd |  | 269 | AATGCCCTTAATGGGAACGGGATCCAATAACATGGACAAGAAGCAGTTAACTGTTATAGG       | 328 |
| Qy |  | 428 | AGGCUAGAGAGGAGNAUACCUIUACCGCGCCACGGAGAUACGCCUGAGCUACAGCGCC         | 487 |
| Dd |  | 329 | AAGCTCAAGAGGGAGATAACTTCCATTGGGGCCAAAGAAATCTCACCTCAGTTATTCGTCT      | 388 |
| Qy |  | 488 | GCGCGCCUGGCCAGCUGCAUGGGCCUGAUCAACACAGGAUGGGCGCGUGACACCCGAG         | 547 |
| Dd |  | 389 | GGTGCACTTGCCAGTTGTATGGCCCTCATATACAAACAGGATGGGGCTGTGACCACTGAA       | 448 |
| Qy |  | 548 | GUGGCCUUCGGCCUGGUGUGGCCACUUGCGAGCAGAUUGC CGCAGCAGCAGCAGCCGAGC      | 607 |
| Dd |  | 449 | GTGGCAATTTGGGCTCGTATGTGTGTCAACTGTGTGAACAGATTTGTGATCTCCAGCACTCGGTCT | 508 |
| Qy |  | 608 | CACAGSCAUAUGGUGACCAACCAACCCCUAGUACAGGCACGAGAACAGCAUGGUGUCUG        | 667 |
| Dd |  | 509 | CATAGGCAATGGTGACAAACCAATCCACTATATCAGATGAGAAACAGAAATGGTTTTA         | 568 |
| Qy |  | 668 | GCAGACCAACCGCCCAAGGCCAUGAGCAGAGUGGCCGCGCAGCAGCAGCGCGCCGAG          | 727 |
| Dd |  | 569 | GCCAGCACTACAGCTAAGGCTATGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG        | 628 |
| Qy |  | 728 | GCAUGGAGUGGCCCGACCGCAGGCGAGAUUGGUGCAGGCCAUGAGGACCAUCCGACCC         | 787 |
| Dd |  | 629 | GCCATGGAGGTTGCTAGTCAGGCTAGACAAAATGGTGCAAGCGATGAGAAACCATTTGGGACT    | 688 |
| Qy |  | 788 | CACCCACAGCAGCAGCGCGCCCUAGAAACCAACCCUUGCUGGAGAACCUAGCGGCCUACCAG     | 847 |
| Dd |  | 689 | CATCTTAGCTCCAGTGTCTGGTCTGAAAAATGATCTTCTTGAANAATTTTGCAGGGCTATCAG    | 748 |
| Qy |  | 848 | AAGCGCAUGGGCGUGCAGAUAGCAGCGCCUUCAAAGUGAAC                          | 895 |
| Dd |  | 749 | AAACGAAATGGGGTGCAGATGCAACGGTTTCAAGTGATC                            | 786 |

## RESIN.T 9

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US-11-131-479-45
; Sequence 45, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Influenza A Virus M1 Fused to Synthetic H5cAg
US-11-131-479-45

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Query Match 46.8%; Score 473; DB 12; Length 1305;  
Best Local Similarity 64.9%; Pred. No. 2.8e-47;  
Matches 489; Conservative 89; Mismatches 175; Indels 0; Gaps 0;

DEC 11 1964

```

RESULDI 10
US-11-155-478A-131
; Sequence 131, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
;
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND CURE
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 987
; TYPE: DNA
; ORGANISM: human Influenza A virus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(987)
; OTHER INFORMATION: human Influenza A virus
; OTHER INFORMATION: strain A/Charlottesville/31/95 (H1N1)
; OTHER INFORMATION: accession number af398876
US-11-135-478A-131

Query Match      45.5%; Score 460.4; DB 12; Length 987;
Best Local Similarity 63.9%; Pred. No. 8.5e-46;
Matches 484; Conservative 88; Mismatches 186; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGGAGACCUAGUGUGUGAGCAUCAUCCCGAGGCGCCCGCUGAAG 187
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 AGTCTTCTAACCGAGGTGGAACGTAGCTTCTCTATCGTCCGTCAGGCGCCCTCAA 63

Qy 188 GCCGAGAUCCGCCAGAGCGGAGGAGUGUUCGCCGACAGACCGACCGACCGUGGUG 247
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCTGGAAGAACACCGATCTTGAGGCT 123

Qy 248 CUGAUGGAGUGGUGAAGACAGGCGCCCAUCCUGAGCGCCCGCUGACCAAGGCGCAUCUGGGC 307
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 CTCATGAGTGCTTAAGACAAGACCGATCTCTGTCACCTCTGACTAAGGGATTTAGGA 183

Qy 308 UUCGUGUACCCUGACCGUGCCCGAGCGAGCGCGGCTGUGAGCGCCCGCUGUGUGAG 367
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 TTTGTGTTCACTGCTTGTATGGGCTCATATACAAAGGATGCGAGCGCTTTGTCAA 243

Qy 368 AACCCCGUAGCGCAAGCGGCGCCCAACAAUGAGCAAGCGCGGUGAGCGUGACG 427
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 AATGCCCTTAATGGGAATGGGGATCCAAATAAATGACAGAGCAGTTAAATCTATAGA 303

Qy 428 AAGCUGAAGAGGAGAUCAUCCUACGCGCCCAAGGAGAUCAUCCUGACUACAGCGCC 487
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 AAGCTTAAGAGGAGATTAATTCATTCATGGGCGCAAGAAATAGCACTCAGTTATCTGCT 363

Qy 488 GCGCGCCUGGCGAGCGUGGCGUGAUCUACAAAGGAGUGGCGCGCGUGACCGCGAG 547
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
364 GGTGCACTTGCCAGTTGATGGGCTCATATACAAAGAAATGGGGCTGTAACCACTGAA 423

Qy 548 GUGGCUUCCGCGUGGUGCGCCACUUGCGAGCAGUCCCGACCGACCGACCGCGAGC 607
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
424 TCAGCATTTGSCCTGATATGCGCAACCTGTGAAACAGATTGCTGCTCCAGCATTAAGTCT 483

Qy 608 CACAGGAGAUUGGUGACCAACCAACCCUUGAUCAGGCGACGAGACAGAGUUGUGUG 667
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
484 CATAGGCAATTTGGTAACAAACCAATTCATTAAATAGACATGAGAACAGAAATGGTCTG 543

Qy 668 GCCAGCACTACAGCTAAAGCTATGAGCAATATGCTGATGAGTGAACAGCACTGAG 727
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
544 GCCAGCACTACAGCTAAAGCTATGAGCAATATGCTGATGAGTGAACAGCACTGAG 603

Qy 728 GCCAUGGAGUGGCGAGCGAGCGAGGAGUUGGUGAGCGGCAUGAGGACCAUCCGCGACC 787
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
604 GCCATGAGGATTTGCTAGTCAAGGCGAGCAATATGCTGAGGCAATGAGAGCCATTTGGGACT 663

Qy 788 CACCCAGCAGCAGCGCGCGCGUAGAAACGACUUGUGGAGACCTUGCAGGCGCUUACCG 847
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
664 CATCTAGCTCTAGACTGGTCTGAAAATGATCTTTTGAATTTTTCAGGCGCTATCAG 723

Qy 848 AAGCGCAUGGCGGCGAGUAGCAGCGCUUCAAAGUGAAC 885
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
724 AAACGAATGGGGTGCAGATGCACGATTAAGTGATC 761

RESULT 11
US-11-131-479-60
; Sequence 60, Application US/11131479
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Db      664  CATCTAGCTCCAGTGTGGTCTAAAGATGATCTTCTGAAATTTGCAGACCTATCAG 723
Qy      848  AAGCGCAUGGCGUGCAGAGCAGCGUCUUAAGUGAAC 885
Db      724  AAACGATGGGGTGCAGATGCAACGATTCAAGTGACC 761

RESULT 12
US-11-131-479-95
; Sequence 95, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4764, Ligation of VR4756 RV-Sali into VR10682 RV
US-11-131-479-95

Query Match      44.9%; Score 454; DB 12; Length 4822;
Best Local Similarity 63.2%; Pred. No. 3.5e-45;
Matches 479; Conservative 89; Mismatches 190; Indels 0; Gaps 0;

Qy      128  AGCCUGUGACCGGAGGAGACCUAGCGUGAGCAUCCGCCAGCGGCCCGCUAGAAG 187
Db      817  AGCTTTTAAACCGAGGTGAAACGTATGTTCTCTATCGTTCCATCAGGCCCTCAA 876
Qy      188  GCCGAGAUCCGCCAGGCGGAGACGUGUUGCGCGCAAGAACACCGACCUAGGUG 247
Db      877  GCCGAAATCGCGAGAGACTTGAAGATGTTCTTTGCGGAAAAACACAGATCTTGAG 936
Qy      248  CUGAUGAGUGGUGAGACGAGCCCAUCCUGAGCCCGGACCAAGGGAUCCUGGCG 307
Db      937  CTCATGGAATGGCTAAAGACAAGACCAATCTCTGTCACCTTGACTAAGGGGATTTTGGG 996
Qy      308  UUCGUGUACCGUACCGCGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db      997  TTTGTGTTACGCTCACCCTGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1056
Qy      368  AACGCCCUUAGCGCAACCGCGACCCCAACCAAGGACCAAGGCGGUGAAGCUGUAC 427
Db      1057  AATGCCCTCAATGGGAATGGGATCCAAATAACATGAGACAGAGCTTAAACTATAGA 1116
Qy      428  AAGCUGAAGAGGAGAGACCUUCCACGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
Db      1117  AAACCTTAAGAGGGAGATTACATTTCCATGGGGCCAAAGAAATAGCACTCAGTTA 1176
Qy      488  GCGCGCGUGGCGAGCUGAUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 547
Db      1177  GGTGCACTTGCAGTTGATGGGCTCTATATACAAAGATGGGGCTGTAACTACTGAA 1236
Qy      548  GUGGCUUUGCGGCGUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
Db      1237  GTGGCCTTTGGCTGTATGTGCAACATGTGAACAGATTGCTGACTCCCGACACAG 1296
Qy      608  CACAGGAGUGGUGACCAACCAACCAACCCCGCGCGCGCGCGCGCGCGCGCGCG 667
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Db      1297  CATAGGCAATGGTGGCAACAACAATCCATTAAAGGCATGAGAACAAGATGTTTGT 1356
Qy      668  GCAGGACACACCCCAAGGCCAUGGAGCAGUGGCGCGCGCGCGCGCGCGCGCGCG 727
Db      1357  GCCAGCACTACAGCTAAGGCTATGAGCAATGGCTGGATCAAGTGAGCAGCGCGGAG 1416
Qy      728  GCCAUGGAGGUGGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 787
Db      1417  GCCATGGAATTTCTAGTCAGGCCAGGCAATGGTCAGGCAATGAGGCATTTGGGACT 1476
Qy      788  CACCCGAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db      1477  CATCTAGCTCCAGTGTGGTCTTAAAGATGATCTTCTTGAATTTGCAGACCTATCAG 1536
Qy      848  AAGCGCAUGGCGUGCAGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 885
Db      1537  AAACGAAATGGGGTGCAGATGCAACGATTCAAGTGACC 1574

RESULT 13
US-11-131-479-101
; Sequence 101, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101
; LENGTH: 5161
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4770, M2 Insert Replacing WNV Insert in VR6430
US-11-131-479-101

Query Match      44.9%; Score 454; DB 12; Length 5161;
Best Local Similarity 63.2%; Pred. No. 3.5e-45;
Matches 479; Conservative 89; Mismatches 190; Indels 0; Gaps 0;

Qy      128  AGCCUGUGACCGGAGGUGAGACCUAGCGUGAGCAUCCGCCAGCGGCCCGCUAGA 187
Db      1150  AGCCTTTAAACCGAGGTGAAACGTATGTTCTCTATCGTTCCATCAGGCCCTCAA 1209
Qy      188  GCCGAGAUCCGCCAGGCGGAGACGUGUUGCGCGCAAGAACACCGACCUAGGUG 247
Db      1210  GCCGAAATCGCGAGAGACTTGAAGATGTTCTTGTGCGGAAAAACACAGATCTTGAG 1269
Qy      248  CUGAUGAGUGGUGGAGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
Db      1270  CTCATGGAATGGCTTAAAGACAAGACCAATCTCTGTCACCTCTGACTAAGGGGATTTGGG 1329
Qy      308  UUCGUGUACCGUACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db      1330  TTTGTGTTACGCTCACCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1389
Qy      368  AACGCCCUUAGCGCAACCGCGACCCCAACCAAGGACCAAGGCGCGCGCGCGCG 427
Db      1390  AATGCCCTCAATGGGAATGGGATCCAAATAACATGAGCAGAGCTTAACTATAGA 1449
Qy      428  AAGCUGAAGAGGAGAGACCUUCCACGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
Db      1450  AAACCTTAAGAGGGAGATTACATTTCCATGGGGCCAAAGAAATAGCACTCAGTTA 1509
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[illegible]

Search completed: March 21, 2006, 01:31:39  
Job time : 461.616 secs